Zara, J.
09/896692

FILE 'REGISTRY' ENTERED AT 10:05:38 ON 30 MAY 2003
L1 300 S TCGCACCCATCTCTCTCCTTCT/SQSN
L2 291 S L1 AND SQL=<100

FILE 'HCAPLUS' ENTERED AT 10:06:56 ON 30 MAY 2003
L3 109 S L2

L5 24 SEA ABB=ON PLU=ON L3(L)(HIV OR HUMAN(3W)VIRUS OR HTLV# OR AIDS OR ACQUIRED(2W)SYNDROM?)

L5 ANSWER 1 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:723747 HCAPLUS
DOCUMENT NUMBER: 136:406717
TITLE: Inhibition of HIV-1 in cell culture by oligonucleotide-loaded nanoparticles
AUTHOR(S): Berton, Myriam; Turelli, Priscilla; Trono, Didier; Stein, Cy A.; Allemann, Eric; Gurny, Robert
CORPORATE SOURCE: School of Pharmacy, University of Geneva, Geneva, CH-1211, Switz.
SOURCE: Pharmaceutical Research (2001), 18(8), 1096-1101
CODEN: PHREEB; ISSN: 0724-8741
PUBLISHER: Kluwer Academic/Plenum Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The potential use of polymeric nanoparticles for the delivery of antisense oligonucleotides in HIV-1-infected cell cultures was investigated. Phosphorothioate oligonucleotides were encapsulated into poly (D,L-lactic acid) nanoparticles. Two models of infected cells were used to test the ability of nanoparticles to deliver them. HeLa P4-2 CD4+ cells, stably transfected with the .beta.-galactosidase reporter gene, were first used to evaluate the activity of the oligonucleotides on a single-round infection cycle. The acutely infected lymphoid CEM cells were then used to evaluate the inhibition of the viral prodn. of HIV-1 by the oligonucleotides. The addn. to infected CEM cells of nanoparticles contg. gag antisense oligonucleotides in the nanomolar range led to strong inhibition of the viral prodn. in a concn.-dependent manner. Similar results were previously obsd. in HeLa P4-2 CD4+ cells. Nanoparticle-entrapped random-order gag oligonucleotides had similar effects on reverse transcription. However, the reverse transcriptase activity of infected cells treated with nanomolar concns. of free antisense and random oligonucleotides was not affected. These results suggest that poly (D,L-lactic acid) nanoparticles may have great potential as an efficient delivery system for oligonucleotides in HIV natural target cells, i.e., lymphocytic cells.
IT **153021-75-1**, GEM91
RL: BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PYP (Physical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(inhibition of **HIV**-1 in cell culture by oligonucleotide-loaded nanoparticles)
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 24 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:605304 HCAPLUS
DOCUMENT NUMBER: 134:25093
TITLE: Evaluation of the binding between potential anti-HIV DNA-based drugs and viral envelope glycoprotein gp120 by capillary electrophoresis with laser-induced fluorescence detection
AUTHOR(S): Zhou, Wei; Tomer, Kenneth B.; Khaledi, Morteza G.
CORPORATE SOURCE: Department of Chemistry, North Carolina State University, Raleigh, NC, 27695-8204, USA
SOURCE: Analytical Biochemistry (2000), 284(2), 334-341
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fusion of the human immunodeficiency virus (HIV) with the target cell was assisted by the interaction between the viral envelope glycoprotein HIV-1 gp120 and a chemokine receptor. Studies have shown that the efficiency of the binding depends on the presence of the V3 loop of the gp120 which is known to interact with polyanions, such as phosphorothioate oligodeoxynucleotides (Sd, potential anti-HIV drugs). In this study, capillary electrophoresis with laser-induced fluorescence detection (CE-LIF) was used to systematically evaluate binding between Sd and HIV-1 gp120. A 25-mer fluorescently tagged phosphorothioate oligodeoxynucleotide (GEM) was employed as a probe to study this interaction. The dissocn. const. (Kd) between GEM and gp120 was detd. to be 0.98 nM by Scatchard anal. The competition consts. (Kc) of a set of Sd that compete with GEM for binding to gp120 were also detd. The results showed that the interaction had a strong dependence on the sulfur phosphorothioate backbone. Chain length and the sequence of Sd also affect the ability of binding to gp120. The ability to study the protein-drug binding in the soln. with minimal sample consumption makes CE-LIF very attractive for biol. studies. (c) 2000 Academic Press.

IT **153021-75-1D**, 5'-fluorescein-labeled
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(binding between potential anti-**HIV** DNA-based drugs and viral envelope glycoprotein gp120)

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:9417 HCAPLUS
DOCUMENT NUMBER: 132:160829
TITLE: Cell binding, uptake and cytosolic partition of HIV anti-gag phosphodiester oligonucleotides 3'-linked to cholesterol derivatives in macrophages
AUTHOR(S): LeDoan, Trung; Etore, Florence; Tenu, Jean-Pierre; Letourneux, Yves; Agrawal, Sudhir
CORPORATE SOURCE: Laboratoire de Biochimie des Transports Cellulaires, CNRSUMR8619, Universite de Paris XI, Orsay, 91405, Fr.
SOURCE: Bioorganic & Medicinal Chemistry (1999), 7(11), 2263-2269

CODEN: BMECEP; ISSN: 0968-0896
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The purpose of this study is to evaluate the cell interactions of a new class of compds. composed of phosphodiester oligonucleotides linked to the cholesterol group at position 3, 7, or 22 of the steroid structure. The resulting conjugates were assessed for their capacity to bind, penetrate and partition in the cytoplasmic compartment of murine macrophages. The results showed that lipophilic conjugates bind to cells much faster (t1/2 .ltoreq.10 min) than do underivatized oligomers. Oligomers tethered to the cholesterol at positions 3 and 7 (PO-GEM-3-Chol and PO-GEM-7-Chol) interacted more efficiently with cell membranes and were better internalized than oligomers attached to the cholesterol moiety at position 22 (PO-GEM-22-Chol). The cytosolic fraction of internalized oligomers was studied by a digitonin-based membrane permeabilization method. The recovered fraction of oligomers that can freely diffuse from the cytosol was comparable for GEM-91, a phosphorothioate congener, and for PO-GEM-7-Chol (50-60% of the internalized oligomers), while that of PO-GEM-3-Chol was less (30% of the internalized oligomers) indicating a higher membrane affinity of the latter deriv. as compared to the other investigated compds. Membrane binding and cell internalization correlated well with the hydrophobicity of the conjugates as characterized by their partition coeffs. in a water-octanol system. Due to their capacity of rapid binding and cytosolic partition in cells, cholesterol-derivatized oligonucleotides at position 3 or 7 of the steroid mol. appeared as good candidates for systemic delivery of anti-HIV antisense compds.

IT **153021-75-1**, GEM-91 **259075-60-0**
259075-61-1 259075-62-2 259075-63-3
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(cell binding, uptake and cytosolic partition of **HIV** anti-gag phosphodiester oligonucleotides 3'-linked to cholesterol derivs. in macrophages)

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:189236 HCAPLUS
DOCUMENT NUMBER: 130:233230
TITLE: Compositions and methods for the identification and quantitation of deletion sequence oligonucleotides in synthetic oligonucleotide preparations
INVENTOR(S): Chen, Danhua; Srivatsa, G. Susan
PATENT ASSIGNEE(S): Isis Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 163 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9911820 A1 19990311 WO 1998-US18084 19980901
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9891278 A1 19990322 AU 1998-91278 19980901
PRIORITY APPLN. INFO.: US 1997-923771 19970902
WO 1998-US18084 19980901

AB The invention provides compns. and methods for the identification and quantitation of a mixt. of various deletion sequence oligonucleotides present in a prepn. of a synthetic oligonucleotide. In a synthetic prepn. of oligonucleotides, yield of full-length products is less than 100% and decreases as n (the no. of nucleobases in the full-length oligonucleotide) increases. Oligonucleotides shorter than the desired full-length oligonucleotide are possibly undesirable impurities. (n-1) type impurities can be classified as terminal deletion or internal deletion sequences, depending upon the position of the missing base. In the methods of the invention, a soln. comprising a mixt. of various deletion sequence oligonucleotides that have been detectably labeled is contacted to a compn. comprising a series of immobilized probes, each probe having a nucleobase sequence that is the reverse complement of a given (n-1) deletion sequence oligonucleotide and wherein a probe is present for every possible (n-1)-mer that can be present in a prepn. of a synthetic oligonucleotide of length n. Unbound oligonucleotides (full-length and other deletion sequences) can be removed from the hybridization reaction by washing, and the (n-1)-mers can be further identified and quantified.

IT **148267-87-2 153021-75-1**, GEM 91
156718-18-2 156718-19-3 156718-20-6
156718-21-7 156718-22-8 156718-23-9
156718-24-0
RL: ARU (Analytical role, unclassified); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(oligonucleotide targeted to **HIV**-1 gag gene; identification and quantitation of deletion sequence oligonucleotides in synthetic oligonucleotide prepns.)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:139949 HCAPLUS
DOCUMENT NUMBER: 130:191877
TITLE: Novel HIV-specific synthetic antisense oligonucleotides and methods of their use
INVENTOR(S): Agrawal, Sudhir
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 64 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9909154	A2	19990225	WO 1998-US16345	19980805
WO 9909154	A3	19990506		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2300352	AA	19990225	CA 1998-2300352	19980805
AU 9887713	A1	19990308	AU 1998-87713	19980805
EP 1007657	A2	20000614	EP 1998-939243	19980805
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001514884	T2	20010918	JP 2000-509820	19980805
US 2002168340	A1	20021114	US 2001-837806	20010418
US 2003100521	A1	20030529	US 2001-896692	20010629

PRIORITY APPLN. INFO.: US 1997-914827 A 19970819
WO 1998-US16345 W 19980805

AB Disclosed are synthetic oligonucleotides having a nucleotide sequence specifically complementary to nucleotides 324-345 of a conserved gag region of the HIV-1 genome, the oligonucleotide consisting of 21 nucleotides which are linked via phosphorothioate internucleotide linkages and optionally contg. 5'- and 3'-terminal 2'-O-methylribonucleotide residues. Also disclosed are methods for inhibiting and treating HIV-1 and HIV-2 infection. To det. the preclin. range of anti-HIV activity of various oligonucleotides, evaluations were performed against a variety of wild-type and drug-resistant strains of HIV-1, including both lab. derived and low passage, clin. strains of virus and T-lymphocyte-tropic and monocyte-macrophage-tropic viruses. The oligonucleotides remained active against viruses resistant to nevirapine, 3TC and protease inhibitors, but were less active against viruses with mutations conferring resistance to AZT. High test concns. exhibited no toxicity even after 14 days, and the oligonucleotides are i.v. and orally bioavailable to rats and monkeys after a single dose. The phosphorothioated oligonucleotide 5'-ucgcacccatctctctccuuc-3' (with the four 5' and the four 3' residues comprising 2'-O-methylribonucleotides) inhibits viral infection or post-viral adsorption with IC50 = 410 nM and IC90 = 1737 nM.

IT **197831-53-1**, GenBank I49132
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(gag region target; **HIV**-specific synthetic antisense oligonucleotides and methods of their use)

L5 ANSWER 6 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:26511 HCAPLUS
DOCUMENT NUMBER: 130:231953
TITLE: Sequence-specific RNase H cleavage of gag mRNA from HIV-1 infected cells by an antisense

oligonucleotide in vitro

AUTHOR(S): Veal, Gareth J.; Agrawal, Sudhir; Byrn, Randal A.

CORPORATE SOURCE: Divisions of Hematology, Oncology and Experimental Medicine, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, MA, 02215, USA

SOURCE: Nucleic Acids Research (1998), 26(24), 5670-5675
CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have used a RNase protection assay to investigate RNase H cleavage of HIV-1 mRNA mediated by phosphorothioate antisense oligonucleotides complementary to the gag region of the HIV-1 genome in vitro. Cell lysate expts. in H9 and U937 cells chronically infected with HIV-1 IIIB showed RNase H cleavage of unspliced gag message but no cleavage of spliced message which did not contain the target gag region. RNase H cleavage products were detected at oligonucleotide concns. as low as 0.01 .mu.M and the RNase H activity was seen to be concn. dependent. Similar expts. with 1-, 3- and 5-mismatch oligonucleotides demonstrated sequence specificity at low concns., with cleavage of gag mRNA correlating with the predicted activities of the parent and mismatch oligonucleotides based on their hybridization melting temps. Expts. in living cells suggested that RNase H-specific antisense activity was largely detd. by the amt. of oligonucleotide taken up by the different cell lines studied. RNase H cleavage products were detected in antisense oligonucleotide treated MT-4 cells acutely infected with HIV-1 IIIB, but not in infected H9 cells treated with oligonucleotide under the same conditions. The data presented demonstrate potent and specific RNase H cleavage of HIV-1 mRNA mediated by an antisense oligonucleotide targeted to HIV-1 gag mRNA, and are in agreement with previous reports that the major obstacle to demonstrating antisense activity in living cells remains the lack of penetration of these agents into the desired cellular compartment.

IT **153021-75-1**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(sequence-specific RNase H cleavage of gag mRNA from **HIV** -1 infected cells by an antisense oligonucleotide in vitro)

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 24 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:409757 HCAPLUS

DOCUMENT NUMBER: 129:144469

TITLE: Antisense oligonucleotide-based therapy for HIV-1 infection from laboratory to clinical trials

AUTHOR(S): Agrawal, Sudhir

CORPORATE SOURCE: Hybridon, Inc., Cambridge, MA, 02142, USA

SOURCE: Clinical Trials of Genetic Therapy with Antisense DNA and DNA Vectors (1998), 331-352.
Editor(s): Wickstrom, Eric. Dekker: New York, N. Y.
CODEN: 66HPAS

DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 39 refs. This chapter discusses GEM 91, a 25-mer oligodeoxynucleoside phosphorothioate designed to bind to the initiation sit of gag mRNA of HIV-1. Targets of GEM 91 during the HIV replication cycle, its antiviral activity in vitro, and experience from administration to rats and monkeys and in human clin. trials are discussed.
IT **153021-75-1**, GEM 91
RL: ADV (Adverse effect, including toxicity); BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide-based therapy for **HIV**-1 infection in lab. animals and humans)
REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:292803 HCAPLUS
DOCUMENT NUMBER: 129:75818
TITLE: Early clinical trials with GEM 91, a systemic oligodeoxynucleotide
AUTHOR(S): Martin, R. Russell
CORPORATE SOURCE: Hybridon, Inc., Cambridge, MA, 02139, USA
SOURCE: Applied Antisense Oligonucleotide Technology (1998), 387-393. Editor(s): Stein, C. A.; Kreig, Arthur M. Wiley-Liss: New York, N. Y. CODEN: 65ZQAC
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 9 refs. on the design and safety and pharmacokinetic trials of the anti-HIV-1 drug GEM 91.
IT **153021-75-1**, GEM 91
RL: ADV (Adverse effect, including toxicity); BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(clin. trials of the anti-**HIV**-1 oligodeoxynucleotide GEM 91)
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 9 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:230586 HCAPLUS
DOCUMENT NUMBER: 129:12318
TITLE: Synergistic inhibition of HIV-1 by an antisense oligonucleotide and nucleoside analog reverse transcriptase inhibitors
AUTHOR(S): Veal, Gareth J.; Agrawal, Sudhir; Byrn, Randal A.
CORPORATE SOURCE: Beth Israel Deaconess Medical Center, Divisions of Hematology/Oncology and Experimental Medicine, Harvard Medical School, Boston, MA, 02215, USA
SOURCE: Antiviral Research (1998), 38(1), 63-73

CODEN: ARSRDR; ISSN: 0166-3542
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have studied the effects of the gag antisense phosphorothioate oligonucleotide GEM 91 and mismatch antisense controls on the antiviral activities of ddC and other nucleoside analogs in HIV-infected MT-4 cells using a cytoprotection based assay. Under std. assay conditions, i.e. simultaneous incubation of drugs, HIV-1 IIIB and MT-4 cells, both GEM 91 and mismatch controls interacted synergistically with ddC resulting in an approx. 40-fold decrease in the IC50 value of ddC; this suggests a potent but sequence non-specific effect of GEM 91. Under post-adsorption assay conditions, i.e. pre-incubation of virus and cells and removal of excess HIV before drug addn., GEM 91 exhibited synergism with ddC, with an approx. 5-fold decrease in ddC IC50 value. This favorable interaction was not seen with any of the mismatch oligonucleotides, suggesting the involvement of a sequence-specific mechanism of action. Similar results were seen with the thymidine analogs AZT and d4T in combination with GEM 91. These data suggest a potential role for GEM 91 and future sequence-specific antisense drugs in combination with nucleoside analogs for the treatment of HIV infection. It is essential that potential interactions between new and existing classes of anti-HIV drugs are studied extensively as antiretroviral drug combinations become increasingly more complex.
IT **153021-75-1**, GEM 91
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(synergistic inhibition of **HIV**-1 by an antisense phosphorothioate oligonucleotide and nucleoside analog reverse transcriptase inhibitors)
REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 10 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:89349 HCAPLUS
DOCUMENT NUMBER: 128:162876
TITLE: Antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans
INVENTOR(S): Schechter, Paul J.; Martin, B. Russel; Tournerie, Christophe; Agrawal, Sudhir
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 93 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9803646	A1	19980129	WO 1996-US12056	19960722

W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO,

RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9665924 A1 19980210 AU 1996-65924 19960722
PRIORITY APPLN. INFO.: WO 1996-US12056 19960722

AB The present invention provides therapeutic compns. and methods for treating humans suffering from diseases or disorders caused by cellular expression of aberrant exogenous genes or aberrant endogenous genes comprising administering to the human a therapeutically effective amt. of an oligonucleotide capable of specifically down-regulating the expression of such a gene. Thus, oligodeoxyribonucleotides are provided which are antisense to residues 324-348 of the conserved gag gene region of human immunodeficiency virus type 1 (HIV-1). These antisense oligonucleotides are more specific, less toxic, and have greater nuclease resistance than many other chemotherapeutic agents designed to inhibit HIV-1 replication. In addn., they are more active in inhibiting viral replication than other known antisense oligonucleotides contg. less than the 324-348 HIV-1 gag sequence. The efficacy and pharmacokinetics profile of phosphorothioated 5'-ctctcgcacccatctctctccttct-3' in the treatment of HIV-1-infected human cell lines are described.

IT **156718-23-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 321-350 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **156718-21-7**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 322-349 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **156718-22-8**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 322-350 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **202833-93-0**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 322-351 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **156718-18-2**
RL: BAC (Biological activity or effector, except adverse); BSU

(Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 323-348 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **156718-20-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 323-349 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **148267-87-2**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 323-350 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **151285-76-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 324-348 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

IT **156718-19-3**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligo antisense to residues 324-349 of **HIV**-1 virus gag gene; antisense oligonucleotides and methods for treating specific gene expression-related diseases and disorders in humans)

REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 11 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:31391 HCAPLUS
DOCUMENT NUMBER: 128:84382
TITLE: Antisense oligonucleotides down-regulating gene expression and their use in the treatment of disease
INVENTOR(S): Schechter, Paul J.; Martin, R. Russell; Tournerie, Christophe; Agrawal, Sudhir; Coombs, Robert W.
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 85 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9748795	A2	19971224	WO 1997-US10143	19970611
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9733096	A1	19980107	AU 1997-33096	19970611
PRIORITY APPLN. INFO.:			US 1996-20417P P	19960618
			WO 1997-US10143 W	19970611

AB Methods of using antisense oligonucleotides to down-regulate gene expression in the control of infection or other diseases are described. A specific example is given for the treatment of HIV infections. Phosphorothioate oligonucleotides directed against the gag gene of HIV-1 were prepd. by std. chem. and their effectiveness tested using std. assays of HIV-1 growth and replication. In an in vitro syncytia inhibition assay, two of these oligonucleotides had EC50's of 1.81 and 1.41 .mu.g/mL. In cytopathic assays, EC50's of 2.54 and 7.75 .mu.g/mL were obsd. Human subject studies are described.

IT **151285-76-6D**, phosphorothioate bond-contg.,
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense DNA to **HIV**-1 gag gene; antisense oligonucleotides down-regulating gene expression and their use in treatment of disease)

L5 ANSWER 12 OF 24 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:	1997:337929 HCAPLUS
DOCUMENT NUMBER:	127:13045
TITLE:	The multiple inhibitory mechanisms of GEM 91, a gag antisense phosphorothioate oligonucleotide, for human immunodeficiency virus type 1
AUTHOR(S):	Yamaguchi, Koushi; Papp, Bela; Zhang, Dezhen; Ali, Ahmad N.; Agrawal, Sudhir; Byrn, Randal A.
CORPORATE SOURCE:	Divisions of Hematology/Oncology and Experimental Medicine, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, MA, 02215, USA
SOURCE:	AIDS Research and Human Retroviruses (1997), 13(7), 545-554 CODEN: ARHRE7; ISSN: 0889-2229
PUBLISHER:	Liebert
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB GEM 91 (gene expression modulator) is a 25-mer oligonucleotide phosphorothioate complementary to the gag initiation site of HIV-1. GEM 91 has been studied in various in vitro cell culture models to examine inhibitory effects on different stages of HIV-1 replication. Expts. were focused on the binding of virions to the cell surface, inhibition of virus entry, reverse transcription (HIV DNA prodn.), inhibition of steady state viral mRNA levels, inhibition of virus

prodn. from chronically infected cells, and inhibition of HIV genome packaging within virions. Expts. were also performed in vitro to generate strains of HIV with reduced sensitivity to GEM 91. The authors obsd. sequence-dependent inhibition of virus entry/reverse transcription and a redn. in steady state viral RNA levels. The authors also obsd. sequence-independent inhibition of virion binding to cells and inhibition of virus prodn. by chronically infected cells. Using in vitro methods that were successful in generating HIV strains with reduced sensitivity to AZT, the authors were unable to generate strains with reduced sensitivity to GEM 91.

IT **153021-75-1**, GEM 91
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(multiple inhibitory mechanisms of gag antisense phosphorothioate oligonucleotide GEM 91 for **human** immunodeficiency **virus** type 1 in relation to resistance)

L5 ANSWER 13 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:253988 HCAPLUS
DOCUMENT NUMBER: 126:235005
TITLE: Method of modifying phosphorothioate oligodeoxyribonucleotides to reduce immunogenicity
INVENTOR(S): Agrawal, Sudhir; Temsamani, Jamal; Zhao, Qiuyan
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9706253	A1	19970220	WO 1996-US11439	19960709
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML				
US 5968909	A	19991019	US 1995-511536	19950804
CA 2229171	AA	19970220	CA 1996-2229171	19960709
AU 9664559	A1	19970305	AU 1996-64559	19960709
EP 850300	A1	19980701	EP 1996-923709	19960709
EP 850300	B1	19991013		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11511014	T2	19990928	JP 1996-508432	19960709
AT 185597	E	19991015	AT 1996-923709	19960709
ES 2141516	T3	20000316	ES 1996-923709	19960709

PRIORITY APPLN. INFO.: US 1995-511536 19950804
WO 1996-US11439 19960709

AB The present invention provides a method of reducing the immunostimulatory effects of certain phosphorothioate

oligonucleotides used to treat pathogen-mediated disease states and other medical conditions. Immunostimulatory effects of phosphorothioate oligonucleotides are reduced by altering, in the 5'- and/or 3'-terminus, the phosphorothioate linkage to a methylphosphonate linkage, or by substituting a ribonucleotide for a deoxyribonucleotide. Phosphorothioate oligonucleotides contg. terminal methylphosphonate linkages or terminal 2'-O-methylribonucleotides induced significantly less splenic cell proliferation and antibody prodn. than did the oligonucleotides contg. only phosphorothioate linkages and no ribonucleotides.

IT **188420-47-5**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(anti-sense oligonucleotide to **HIV**-1 gag gene; method of modifying phosphorothioate oligodeoxyribonucleotides to reduce immunogenicity)

L5 ANSWER 14 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:166407 HCAPLUS
DOCUMENT NUMBER: 126:311756
TITLE: Anti-HIV activities and mechanisms of antisense oligonucleotides
AUTHOR(S): Hatta, Toshifumi; Inagawa, Takabumi; Kuwasaki, Tomoyuki; Kinzuka, Yasuhiro; Takai, Kazuyuki; Yokoyama, Shigeyuki; Nakashima, Hideki; Yamamoto, Naoki; Takaku, Hiroshi
CORPORATE SOURCE: Dep. Industrial Chem., Chiba Inst. Technol., Chiba, Japan
SOURCE: Biotechnologia (1996), (4), 116-131, 1 plate
CODEN: BIECEV; ISSN: 0860-7796
PUBLISHER: Instytut Chemii Bioorganicznej PAN
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We demonstrated that unmodified and modified (phosphorothioate) oligonucleotides prevent cDNA synthesis by the AMV, MMLV, and HIV reverse transcriptases. Antisense oligonucleotide/RNA hybrids specifically arrest primer extension. The blockage involves the degrdn. of the RNA fragment bound to the antisense oligonucleotide by the reverse transcriptase assocd. RNase H activity. However, the phosphorothioate oligomer inhibited polymn. by binding to the AMV and MMLV RTs, rather than to the template RNA, whereas there was no competitive binding of the phosphorothioate oligomer on the HIV RT during reverse transcription. Observation of FITC-S-ODN-rev-treated MOLT-4 cells with a confocal laser scanning microscope, revealed diffuse fluorescence, apparently within the cytoplasm. Interestingly, fluorescent signals were accumulated in the nuclear region of chronically infected MOLT-4/HIV-1 after a 60 min incubation. We also describe the long-term treatment of human immunodeficiency virus-infected cells with antisense phosphorothioate oligonucleotides.

IT **146318-97-0**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(anti-**HIV** activities and mechanisms of antisense oligonucleotides)

L5 ANSWER 15 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:751517 HCAPLUS
DOCUMENT NUMBER: 126:14743
TITLE: Antisense cooperative oligonucleotides for improved inhibition of gene expression
INVENTOR(S): Kandimalla, Ekambar R.; Agrawal, Sudhir
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 84 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9632474	A1	19961017	WO 1996-US4605	19960404
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR				
US 6372427	B1	20020416	US 1995-420672	19950412
AU 9654418	A1	19961030	AU 1996-54418	19960404
US 2003099959	A1	20030529	US 2002-54429	20020122

PRIORITY APPLN. INFO.: US 1995-420672 A 19950412
WO 1996-US4605 W 19960404

AB Disclosed is a compn. comprising at least 2 synthetic, cooperative oligonucleotides, each comprising a region complementary to one of tandem, non-overlapping regions of a target single-stranded nucleic acid, and each further comprising a dimerization domain at a terminus of each of the oligonucleotides, the dimerization domains of the oligonucleotides being complementary to each other. Also disclosed are duplex structures, ternary complexes, pharmaceutical formulations, and methods utilizing the cooperative oligonucleotides of the invention. The antisense oligonucleotides are optimized for therapeutic and diagnostic use and have improved sequence specificity for a single-stranded target, reduced toxicity, and improved biol. activity as antisense mols. The cooperative nature of the described oligonucleotides was demonstrated from (1) thermal melting studies, (2) their ability to activate RNase H, and (3) their ability to inhibit HIV-1 viral gag mRNA expression or influenza gene expression in cell culture. Modified (phosphorothioate internucleotide-linked) oligonucleotide combinations with an extended dimerization domain have an enhanced ability to inhibit the expression of the target gene.

IT **151285-76-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense for **HIV** gag gene; antisense cooperative oligonucleotides for improved inhibition of gene expression)

L5 ANSWER 16 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:683875 HCAPLUS
DOCUMENT NUMBER: 126:70079

TITLE: Mixed backbone antisense oligonucleotides containing 2'-5'-ribo- and 3'-5'-deoxyribonucleosides: synthesis, biochemical and biological properties
AUTHOR(S): Kandimalla, Ekambar R.; Agrawal, Sudhir
CORPORATE SOURCE: Hybridon, Inc., Worcester, MA, 01605, USA
SOURCE: Nucleic Acids Symposium Series (1996), 35(Twentythird Symposium on Nucleic Acids Chemistry, 1996), 125-126
CODEN: NACSD8; ISSN: 0261-3166
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The authors designed and synthesized mixed backbone oligonucleotides (MBOs) contg. 2'-5'-ribo- and 3'-5'-deoxyribonucleosides. Thermal melting studies of the duplexes of MBOs with complementary DNA and RNA target strands suggested that the introduction of 2'-5'-linkages destabilizes the complex with the RNA strand less than the duplex with the DNA strand. The new oligonucleotides were more stable against snake venom phosphodiesterase, S1 nuclease, and fetal calf serum. Phoshorothioate (PS) analogs of MBOs showed activity against HIV-1 in cell cultures comparable to that of a control PS-oligonucleotide.

IT **151285-76-6P 153021-75-1P**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(synthesis of mixed backbone antisense oligonucleotides contg. 2'-5'-ribo- and 3'-5'-deoxyribonucleosides, their biochem. properties, and their inhibition of **HIV**-1 replication)

L5 ANSWER 17 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1995:736756 HCAPLUS
DOCUMENT NUMBER: 123:132062
TITLE: Pharmacokinetics of an anti-human immunodeficiency virus antisense oligodeoxynucleotide phosphorothioate (GEM 91) in HIV-infected subjects
AUTHOR(S): Zhang, Ruiwen; Yan, Jieming; Shahinian, Harout; Amin, Girish; Lu, Zhihong; Liu, Tiepu; Saag, Michael S.; Jiang, Zhiwei; Temsamani, Jamal; et al.
CORPORATE SOURCE: Department Pharmacology Toxicology, University Alabama, Birmingham, AL, USA
SOURCE: Clinical Pharmacology and Therapeutics (St. Louis) (1995), 58(1), 44-53
CODEN: CLPTAT; ISSN: 0009-9236
PUBLISHER: Mosby-Year Book
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Human pharmacokinetics of an antisense oligodeoxynucleotide phosphorothioate (GEM 91) developed as an antihuman immunodeficiency virus (HIV) agent was carried out in this study. 35S-labeled GEM 91 was administered to 6 HIV-infected individuals by means of 2-h i.v. infusions at a dose of 0.1 mg/kg. Plasma disappearance curves for GEM 91-derived radioactivity could be described by the sum of 2 exponentials, with half-life values of 0.18 .+-. 0.04 and 26.71 .+-. 1.67 h. The radioactivity in plasma was further evaluated by

polyacrylamide gel electrophoresis, showing the presence of both intact GEM 91 and lower mol. wt. metabolites. Urinary excretion represented the major pathway of elimination, with 49.15% .+-. 6.80% of the administered dose excreted within 24 h and 70.37% .+-. 6.72% over 96 h after dosing. The radioactivity in urine was assocd. with lower mol. wt. metabolites. No drug-related toxicity was obsd.

IT **170274-79-0**, GEM 91
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(pharmacokinetics of an anti-**human** immunodeficiency **virus** antisense oligodeoxynucleotide phosphorothioate (GEM 91) in **HIV**-infected humans)

L5 ANSWER 18 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:645487 HCAPLUS
DOCUMENT NUMBER: 121:245487
TITLE: Antisense oligodeoxynucleotide phosphorothioate complementary to Gag mRNA blocks replication of human immunodeficiency virus type 1 in human peripheral blood cells
AUTHOR(S): Lisziewicz, Julianna; Sun, Daisy; Weichold, Frank F.; Thierry, Alain R.; Lusso, Paolo; Tang, Jinyan; Gallo, Robert C.; Agrawal, Sudhir
CORPORATE SOURCE: Lab. Tumor Cell Biology, Natl. Cancer Inst., Bethesda, MD, 20892, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1994), 91(17), 7942-6
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Gene-expression modulator 91 (GEM91) is a 25-nt antisense oligodeoxynucleotide phosphorothioate complementary to the Gag mRNA of human immunodeficiency virus type 1 (HIV-1). Cellular uptake and intracellular distribution of GEM91 within cells suggest that this oligomer is readily available for antisense activity. GEM91 inhibited HIV-1 replication in a dose-dependent and sequence-specific manner. In a comparative study, 2 .mu.M GEM91 was as effective as 5 .mu.M 3'-azido-3'-deoxythymidine in blocking virus replication during the 28-day treatment of an HIV-1-infected T-cell line. GEM91 also completely inhibited (>99%) of the growth of three different HIV-1 isolates in primary lymphocytes and prevented the cytopathic effect of the virus in primary CD4+ T cells. Similarly, treatment with GEM91 for 3 wk of HIV-1/BaL-infected primary macrophages blocked virus replication. Based on GEM91 anti-HIV-activity, safety, and pharmacokinetic profile in animals, a clin. trial was started using this compd. as an antisense oligonucleotide drug for the treatment of the acquired immunodeficiency syndrome.

IT **170274-79-0**, GEM 91
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(phosphorothioate-linked antisense oligonucleotide to gag gene of **HIV**-1, for inhibition of replication)

L5 ANSWER 19 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:597667 HCAPLUS
DOCUMENT NUMBER: 121:197667
TITLE: Method of conferring resistance to retroviral

infection
INVENTOR(S): Greatbatch, Wilson; Sanford, John C.
PATENT ASSIGNEE(S): Greatbatch Gen-Aid, Ltd., USA
SOURCE: U.S., 35 pp. Cont.-in-part of U.S. Ser. No. 156,188, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5324643	A	19940628	US 1991-739718	19910729
AT 208813	E	20011115	AT 1989-102692	19890216
US 5580761	A	19961203	US 1994-217210	19940323

PRIORITY APPLN. INFO.: US 1988-156188 B2 19880216
US 1991-739718 A2 19910729

AB A method of conferring resistance to retroviral infection upon a host cell by interfering with one or more of the infection processes including retroviral replication and assembly into infective viral particles is described. The method involves the introduction of a polynucleotide that is transcribed to form a transcript that is complementary or homologous sequence to a viral sequence and interferes with replication or assembly of the retrovirus. Retrovirus resistant cells prepd. by this method can be used in the treatment of retroviral infection. The method is demonstrated using sequences directed against feline leukemia virus to prevent its growth in cultured mink lung cells. Oligonucleotides interfering with the function of the long terminal repeat, the primer binding site, and translation initiation were all shown to slow the rate of virus multiplication.

IT **157909-44-9**
RL: BIOL (Biological study)
(synthetic oligonucleotide interfering with tat transcript splicing and gag gene expression and translation in **human** immunodeficiency **virus**)

L5 ANSWER 20 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:501227 HCAPLUS
DOCUMENT NUMBER: 121:101227
TITLE: Therapeutic anti-HIV oligonucleotide and pharmaceutical
INVENTOR(S): Agrawal, Sudhir; Tang, Jin Yan
PATENT ASSIGNEE(S): Hybridon, Inc., USA
SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9408004	A1	19940414	WO 1993-US9392	19931004

W: AU, BB, BG, BR, CA, CZ, FI, HU, JP, KP, KR, LK, LV, NO, NZ, PL, RO, RU, SD, US
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, PT, SE

EP 664833	A1	19950802	EP 1993-924289	19931004
EP 664833	B1	19961227		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
HU 72400	A2	19960429	HU 1995-995	19931004
JP 08504570	T2	19960521	JP 1993-509354	19931004
AT 146819	E	19970115	AT 1993-924289	19931004
ES 2096343	T3	19970301	ES 1993-924289	19931004
AU 678415	B2	19970529	AU 1994-54028	19931004
AU 9454028	A1	19940426		
BR 9307191	A	19990330	BR 1993-7191	19931004
US 5684147	A	19971104	US 1994-319823	19941007
FI 9501600	A	19950510	FI 1995-1600	19950404
NO 9501307	A	19950601	NO 1995-1307	19950404
PRIORITY APPLN. INFO.:			US 1992-958135 A	19921005
			WO 1993-US9392 W	19931004

AB Disclosed are oligonucleotides having nucleotide sequences that hybridize to at least nucleotides 324 to 348 of a conserved gag region of the HIV-1 genome. These oligonucleotides have about 25 to 30 nucleotides linked by at least one non-phosphodiester internucleotide linkage which render them resistant to nuclease digestion. Also disclosed are therapeutic formulations contg. such oligonucleotides and methods of inhibition HIV-1 proliferation and of treating HIV-1 infection in a mammal. Phosphorothioate-modified oligodeoxynucleotides 25-30 nucleotide in length which hybridize to the specified region of the HIV-1 genome were shown to be more effective that a 20-mer complementary to 327-346 or a 28-mer complementary to only a fragment of the 324-348 region. Syncytia formation, p24 expression, cytopathic effect, and reverse transcriptase activity were monitored to assay the effects of the antisense oligonucleotides.

IT **148267-87-2D**, phosphorothioate-contg. **151285-76-6D**, phosphorothioate-contg. **156718-18-2D**, phosphorothioate-contg. **156718-19-3D**, phosphorothioate-contg. **156718-20-6D**, phosphorothioate-contg. **156718-21-7D**, phosphorothioate-contg. **156718-22-8D**, phosphorothioate-contg. **156718-23-9D**, phosphorothioate-contg. **156718-24-0D**, phosphorothioate-contg.
RL: USES (Uses)
(antisense oligonucleotide complementary to **HIV**-1 gag gene sequence for treatment of **HIV**-1 infection)

L5 ANSWER 21 OF 24 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:	1993:573628 HCAPLUS
DOCUMENT NUMBER:	119:173628
TITLE:	Long-term treatment of human immunodeficiency virus-infected cells with antisense oligonucleotide phosphorothioates
AUTHOR(S):	Lisziewicz, Julianna; Sun, Daisy; Metelev, Valeri; Zamecnik, Paul; Gallo, Robert C.; Agrawal, Sudhir
CORPORATE SOURCE:	Lab. Tumor Cell Biol., Natl. Cancer Inst., Bethesda, MD, 20853, USA
SOURCE:	Proceedings of the National Academy of Sciences of the United States of America (1993), 90(9), 3860-4 CODEN: PNASA6; ISSN: 0027-8424

DOCUMENT TYPE: Journal
LANGUAGE: English
AB The antiviral activity of antisense oligodeoxy-nucleotide phosphorthioates complementary to the tat gene, the gag mRNA, and the rev mRNA were studied in a long-term infection model. Three antisense oligonucleotides directed to the splice-acceptor site of the tat gene failed to suppress human immunodeficiency virus type I replication at 1 .mu.M concn. in the long-term culture. In contrast, two oligodeoxynucleotide phosphorothioates (28-mer) complementary to the gag and the rev mRNAs inhibited viral replication for >80 days, and the antiviral activity was sequence- and length-dependent. In addn., after pretreatment of cells, the authors could reduce the concn. of the antisense oligodeoxynucleotides by >10-fold and still maintain the inhibition of viral replication. These results suggest that chemotherapy for human immunodeficiency virus type 1 infection with antisense oligodeoxynucleotide phoshporothioates may be achieved by an initial high-dose treatment followed by a lower maintenance dose.
IT **148267-87-2**
RL: BIOL (Biological study)
(**human** immunodeficiency **virus** inhibition by, as antisense oligonucleotide)

L5 ANSWER 22 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:462145 HCAPLUS
DOCUMENT NUMBER: 119:62145
TITLE: GEM 91 - an antisense oligonucleotide phosphorothioate as a therapeutic agent for AIDS
AUTHOR(S): Agrawal, Sudhir; Tang, Jin Yan
CORPORATE SOURCE: Hybridon, Inc., Worcester, MA, USA
SOURCE: Antisense Research and Development (1992), 2(4), 261-6
CODEN: AREDEI; ISSN: 1050-5261
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review and discussion with 18 refs.
IT **170274-79-0**, GEM 91
RL: BIOL (Biological study)
(as antisense oligonucleotide phosphorothioate, for treatment of **AIDS**)

L5 ANSWER 23 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:420486 HCAPLUS
DOCUMENT NUMBER: 119:20486
TITLE: Method of inhibiting viral replication, and application to inhibition of human immunodeficiency virus-1 (HIV-1)
INVENTOR(S): Lisziewicz, Julianna; Sun, Daisy M. S.
PATENT ASSIGNEE(S): United States Dept. of Health and Human Services, USA
SOURCE: U. S. Pat. Appl., 31 pp. Avail. NTIS Order No. PAT-APPL-7-906,881.
CODEN: XAXXAV
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 906881	A0	19930401	US 1992-906881	19920702
WO 9401551	A1	19940120	WO 1993-US6380	19930702
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9346664	A1	19940131	AU 1993-46664	19930702
AU 678980	B2	19970619		
EP 649466	A1	19950426	EP 1993-916997	19930702
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				

PRIORITY APPLN. INFO.: US 1992-906881 19920702
WO 1993-US6380 19930702

AB A method is disclosed for selection of drugs suitable for use in inhibiting viral replication in vivo. Also disclosed is a method for inhibiting viral replication using oligonucleotides complementary to specific regions of the genome of the target virus. A culture system is provided that simulates in vivo conditions of viral infection, esp. HIV-1 infection. The culture system can be used to evaluate the long-term efficacy of antiviral drug treatment, e.g. antisense oligonucleotide treatment. The invention further relates to a method of reducing the viral burden in an infected individual. The method involves the sequential treatment of virally infected cells with a combination of different antisense oligonucleotides. The method has the advantage that it prevents the formation of escape mutants of the target virus. The culture system of the invention extends the treatment period over weeks rather than days and therefore permits simulation of a treatment schedule that can be given to a virally infected patient. The methodol. of the invention was used to test the effect of antisense nucleotides (sequences included) on HIV-1 replication in a CD4+ cell line (Molt3) infected with a low multiplicity of infection of HIV-1/IIIB.

IT **148267-87-2D**, phosphorothioate-derivatized
RL: ANST (Analytical study)
(antisense oligonucleotide, **human** immunodeficiency **virus** 1 inhibition with)

L5 ANSWER 24 OF 24 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:116248 HCAPLUS
DOCUMENT NUMBER: 118:116248
TITLE: Specific inhibition of human immunodeficiency virus type 1 replication by antisense oligonucleotides: an in vitro model for treatment
AUTHOR(S): Lisziewicz, Julianna; Sun, Daisy; Klotman, Mary; Agrawal, Sudhir; Zamecnik, Paul; Gallo, Robert
CORPORATE SOURCE: Lab. Tumor Cell Biol., Natl. Cancer Inst., Bethesda, MD, 20892, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1992), 89(23), 11209-13
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have developed a culture system, simulating in vivo conditions of human immunodeficiency virus type 1 (HIV-1) infection, to evaluate the long-term efficacy of antisense oligonucleotide treatment. Five

oligonucleotide phosphorothioates (28-mers), complementary to different regions of HIV-1 RNA, blocked replication of the virus in a sequence-specific manner at 1 .mu.M concn. Variations in antiviral activity were seen among the different oligonucleotides, revealing an effect of target selection. Mismatched or random oligonucleotide phosphorothioates delayed, but did not completely inhibit, HIV-1 replication. In the case of inhibition by a splice-acceptor-site antisense oligodeoxynucleotide, a breakthrough phenomenon occurred after 25 days of treatment, suggesting the development of an "escape mutant". This result did not occur when the inhibitory oligodeoxynucleotides were complementary to the primary-sequence areas of the rev-responsive element and rev-1 genes. Sequential treatment of HIV-1-infected cells with a combination of different antisense oligonucleotides, each administered once, also prevented the development of escape mutants. Results suggest that chemotherapy based on specifically targeted antisense-oligonucleotide phosphorothioates may be an effective method for reducing the viral burden in HIV-1-infected individuals at clin. achievable oligonucleotide concns.

IT **146318-97-0**
RL: BIOL (Biological study)
(**HIV**-1 replication inhibition by)

E1 THROUGH E20 ASSIGNED

FILE 'REGISTRY' ENTERED AT 10:09:59 ON 30 MAY 2003
L6 20 SEA FILE=REGISTRY ABB=ON PLU=ON (153021-75-1/BI OR 148267-87-2/BI OR 151285-76-6/BI OR 156718-18-2/BI OR 156718-19-3/BI OR 156718-20-6/BI OR 156718-21-7/BI OR 156718-22-8/BI OR 156718-23-9/BI OR 170274-79-0/BI OR 146318-97-0/BI OR 156718-24-0/BI OR 157909-44-9/BI OR 188420-47-5/BI OR 197831-53-1/BI OR 202833-93-0/BI OR 259075-60-0/BI OR 259075-61-1/BI OR 259075-62-2/BI OR 259075-63-3/BI)

L7 20 L2 AND L6

L7 ANSWER 1 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **259075-63-3** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T), 3'-[3-[[3-[[(3.beta.)-3-hydroxycholest-5-en-22-yl]amino]-3-oxopropyl]dithio]propyl hydrogen phosphate] (9CI) (CA INDEX NAME)
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:160829

L7 ANSWER 2 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **259075-62-2** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T), 3'-[3-[[(3.beta.)-3-hydroxycholest-5-en-7-yl]dithio]propyl hydrogen

phosphate] (9CI) (CA INDEX NAME)
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:160829

L7 ANSWER 3 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **259075-61-1** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T), 3'-[3-[(3.beta.)-cholest-5-en-3-yldithio]propyl hydrogen phosphate] (9CI) (CA INDEX NAME)
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:160829

L7 ANSWER 4 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **259075-60-0** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T), 3'-[3-(2-pyridinyldithio)propyl hydrogen phosphate] (9CI) (CA INDEX NAME)
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:160829

L7 ANSWER 5 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **202833-93-0** REGISTRY
CN DNA, d(A-C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A-G-C) (9CI) (CA INDEX NAME)
CI MAN
SQL **31**

SEQ 1 acgctctcgc acccatctct ctccttctag c
==== ========== ========
HITS AT: 7-28

REFERENCE 1: 128:162876

L7 ANSWER 6 OF 20 REGISTRY COPYRIGHT 2003 ACS

RN **197831-53-1** REGISTRY
CN DNA, d(T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T) (9CI) (CA INDEX NAME)
CI MAN
SQL **22**

SEQ 1 tcgcacccat ctctctcctt ct
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:191877

L7 ANSWER 7 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **188420-47-5** REGISTRY
CN DNA, d(C-P-deoxy-P-methyl-T-P-deoxy-P-methyl-C-P-deoxy-P-methyl-T-P-deoxy-P-methyl-C-sp-G-sp-C-sp-A-sp-C-sp-C-sp-C-sp-A-sp-T-sp-C-sp-T-sp-C-sp-T-sp-C-sp-T-sp-C-sp-C-P-deoxy-P-methyl-T-P-deoxy-P-methyl-T-P-deoxy-P-methyl-C-P-deoxy-P-methyl-T) (9CI) (CA INDEX NAME)
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 126:277696

REFERENCE 2: 126:235005

L7 ANSWER 8 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **170274-79-0** REGISTRY
CN DNA, d(P-thio)(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T), tetracosasodium salt (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-T-C-T-T-C-T), tetracosasodium salt
OTHER NAMES:
CN Trecovirsen sodium
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 127:28622

REFERENCE 2: 124:277954

REFERENCE 3: 123:132062

REFERENCE 4: 122:255450

REFERENCE 5: 122:95897

REFERENCE 6: 121:245487

REFERENCE 7: 119:62145

L7 ANSWER 9 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **157909-44-9** REGISTRY
CN DNA (synthetic human immunodeficiency virus gene gag/tat expression-inhibiting) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (synthetic human immunodeficiency provirus gene gag/tat expression-inhibiting)
CI MAN
SQL **70**

SEQ 1 tgacgctctc gcacccatct ctctccttct agcctccgct agtcaaaatt
== ========== ==========
51 tttggcgtac tcaccagtcg
HITS AT: 9-30

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:197667

L7 ANSWER 10 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **156718-24-0** REGISTRY
CN DNA, d(A-C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A-G) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(A-C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-C-T-T-C-T-A-G)
CI MAN
SQL **30**

SEQ 1 acgctctcgc acccatctct ctccttctag
==== ========== ========
HITS AT: 7-28

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:233230

REFERENCE 2: 130:129956

REFERENCE 3: 121:101227

L7 ANSWER 11 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **156718-23-9** REGISTRY
CN DNA, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A-G-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-C-T-T-C-T-A-G-C)
CI MAN
SQL **30**

```
SEQ      1 cgctctcgca cccatctctc tccttctagc
               ===== ========== =======
HITS AT:   6-27

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  130:233230

REFERENCE   2:  130:129956

REFERENCE   3:  128:162876

REFERENCE   4:  121:101227

L7   ANSWER 12 OF 20  REGISTRY  COPYRIGHT 2003 ACS
RN   156718-22-8  REGISTRY
CN   DNA, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A-G)
     (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-
     C-T-T-C-T-A-G)
CI   MAN
SQL  29

SEQ      1 cgctctcgca cccatctctc tccttctag
               ===== ========== =======
HITS AT:   6-27

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  130:233230

REFERENCE   2:  130:129956

REFERENCE   3:  128:162876

REFERENCE   4:  121:101227

L7   ANSWER 13 OF 20  REGISTRY  COPYRIGHT 2003 ACS
RN   156718-21-7  REGISTRY
CN   DNA, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A-G)
     (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-
     T-T-C-T-A-G)
CI   MAN
SQL  28

SEQ      1 gctctcgcac ccatctctct ccttctag
              ====== ========== ======
HITS AT:   5-26

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

REFERENCE   1:  130:233230

REFERENCE   2:  130:129956
```

REFERENCE 3: 128:162876

REFERENCE 4: 121:101227

L7 ANSWER 14 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **156718-20-6** REGISTRY
CN DNA, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A)
CI MAN
SQL **27**

SEQ 1 gctctcgcac ccatctctct ccttcta
====== ========== ======
HITS AT: 5-26

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:233230

REFERENCE 2: 130:129956

REFERENCE 3: 128:162876

REFERENCE 4: 121:101227

L7 ANSWER 15 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **156718-19-3** REGISTRY
CN DNA, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T)
CI MAN
SQL **26**

SEQ 1 gctctcgcac ccatctctct ccttct
====== ========== ======
HITS AT: 5-26

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:233230

REFERENCE 2: 130:129956

REFERENCE 3: 128:162876

REFERENCE 4: 121:101227

L7 ANSWER 16 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **156718-18-2** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-

T-C-T-A)
CI MAN
SQL **26**

SEQ 1 ctctcgcacc catctctctc cttcta
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:233230

REFERENCE 2: 130:129956

REFERENCE 3: 128:162876

REFERENCE 4: 121:101227

L7 ANSWER 17 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **153021-75-1** REGISTRY
CN DNA, d(P-thio)(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T)
(9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-
T-C-C-T-T-C-T)
OTHER NAMES:
CN 324-348-Deoxyribonucleic acid (human immunodeficiency virus 1 gene
gag)
CN GEM 91
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:406717

REFERENCE 2: 135:335066

REFERENCE 3: 134:25093

REFERENCE 4: 133:27336

REFERENCE 5: 132:279454

REFERENCE 6: 132:160829

REFERENCE 7: 130:267702

REFERENCE 8: 130:267697

REFERENCE 9: 130:246352

REFERENCE 10: 130:233230

L7 ANSWER 18 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **151285-76-6** REGISTRY
CN DNA, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T)
OTHER NAMES:
CN 6: PN: US6140490 SEQID: 157 unclaimed DNA
CI MAN
SQL **25**

SEQ 1 ctctcgcacc catctctctc cttct
======= ========== =====
HITS AT: 4-25

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:321004

REFERENCE 2: 130:168605

REFERENCE 3: 130:129956

REFERENCE 4: 130:52683

REFERENCE 5: 129:299001

REFERENCE 6: 128:162876

REFERENCE 7: 128:151268

REFERENCE 8: 128:84382

REFERENCE 9: 128:57018

REFERENCE 10: 128:48453

L7 ANSWER 19 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **148267-87-2** REGISTRY
CN DNA, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A)
CI MAN
SQL **28**

SEQ 1 cgctctcgca cccatctctc tccttcta
===== ========== =======
HITS AT: 6-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 130:233230

REFERENCE 2: 130:129956

REFERENCE 3: 128:162876

REFERENCE 4: 121:101227

REFERENCE 5: 119:173628

REFERENCE 6: 119:20486

L7 ANSWER 20 OF 20 REGISTRY COPYRIGHT 2003 ACS
RN **146318-97-0** REGISTRY
CN DNA, d(P-thio)(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(P-thio)(C-G-C-T-C-T-C-G-C-A-C-C-C-A-T-C-T-C-T-C-T-C-C-T-T-C-T-A)
CI MAN
SQL **28**

SEQ 1 cgctctcgca cccatctctc tccttcta
=====
HITS AT: 6-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 126:311756

REFERENCE 2: 118:116248

FILE 'HOME' ENTERED AT 10:10:35 ON 30 MAY 2003

~~9477~~16

Access DB# _____

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MAY 22 2003
TC/CHEM. C...

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5/22/03

Art Unit: 1636 Phone Number 306-5820 Serial Number: 09/896,692

Mail Box and Bldg/Room Location: 11D03 Results Format Preferred (circle): PAPER DISK E-MAIL

↳ 11E12

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Novel HIV oligo's

Inventors (please provide full names): Agrawal et al.

Earliest Priority Filing Date: 8/19/97

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please Searched Seq ID No. 5

Please limit to 100 NT's

Thanks!

5-22 NA

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: Beverly 4994	NA Sequence (#)	STN
Searcher Phone #:	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up:	Bibliographic	Dr.Link
Date Completed: 05-30-03	Litigation	Lexis/Nexis
Searcher Prep & Review Time: 3	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time: 25	Other	Other (specify) CGN

PTO-1590 (8-01)

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 14:49:34 ; Search time 869 Seconds
(without alignments)
736.780 Million cell updates/sec

Title: US-09-896-692B-5
Perfect score: 22
Sequence: 1 tcgcacccatctctctccttct 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	6	I49132	I49132 Sequence 6
2	22	100.0	23	6	I49131	I49131 Sequence 5
3	22	100.0	24	6	I49130	I49130 Sequence 4
4	22	100.0	25	6	AR001561	AR001561 Sequence
5	22	100.0	25	6	AR052661	AR052661 Sequence
6	22	100.0	25	6	AR052662	AR052662 Sequence
7	22	100.0	25	6	AR052663	AR052663 Sequence
8	22	100.0	25	6	AR052664	AR052664 Sequence
9	22	100.0	25	6	AR072068	AR072068 Sequence
10	22	100.0	25	6	AR080760	AR080760 Sequence
11	22	100.0	25	6	AR080761	AR080761 Sequence
12	22	100.0	25	6	AR080762	AR080762 Sequence
13	22	100.0	25	6	AR082591	AR082591 Sequence
14	22	100.0	25	6	AR082592	AR082592 Sequence
15	22	100.0	25	6	AR082593	AR082593 Sequence
16	22	100.0	25	6	AR082594	AR082594 Sequence
17	22	100.0	25	6	AR082595	AR082595 Sequence
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21	22	100.0	25	6	AR082599	AR082599 Sequence
22	22	100.0	25	6	AR082600	AR082600 Sequence
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26	22	100.0	25	6	AR082604	AR082604 Sequence
27	22	100.0	25	6	AR082605	AR082605 Sequence
28	22	100.0	25	6	AR082606	AR082606 Sequence
29	22	100.0	25	6	AR082607	AR082607 Sequence
30	22	100.0	25	6	AR082608	AR082608 Sequence
31	22	100.0	25	6	AR082609	AR082609 Sequence
32	22	100.0	25	6	AR118312	AR118312 Sequence
33	22	100.0	25	6	AR206340	AR206340 Sequence
34	22	100.0	25	6	AX363485	AX363485 Sequence
35	22	100.0	25	6	AX363486	AX363486 Sequence
36	22	100.0	25	6	AX363487	AX363487 Sequence
37	22	100.0	25	6	AX363488	AX363488 Sequence
38	22	100.0	25	6	AX363489	AX363489 Sequence
39	22	100.0	25	6	AX363490	AX363490 Sequence
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42	22	100.0	25	6	AX363493	AX363493 Sequence
43	22	100.0	25	6	AX363494	AX363494 Sequence
44	22	100.0	25	6	AX363495	AX363495 Sequence
45	22	100.0	25	6	AX363496	AX363496 Sequence
46	22	100.0	25	6	AX363497	AX363497 Sequence
47	22	100.0	25	6	AX363498	AX363498 Sequence
48	22	100.0	25	6	AX363499	AX363499 Sequence
49	22	100.0	25	6	AX363500	AX363500 Sequence
50	22	100.0	25	6	AX363501	AX363501 Sequence
51	22	100.0	25	6	AX363502	AX363502 Sequence
52	22	100.0	25	6	I19490	I19490 Sequence 1
53	22	100.0	25	6	I21846	I21846 Sequence 1
54	22	100.0	25	6	I23712	I23712 Sequence 7
55	22	100.0	25	6	I24071	I24071 Sequence 7
56	22	100.0	25	6	I26576	I26576 Sequence 1
57	22	100.0	25	6	I27196	I27196 Sequence 7
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	78	22	100.0	25	6	I58801
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	80	22	100.0	25	6	I58803
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	82	22	100.0	25	6	I72627
	83	22	100.0	25	6	I76420
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	87	22	100.0	27	6	AR170397
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	96	22	100.0	30	6	I72634
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	102	22	100.0	35	6	I07197
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	104	22	100.0	37	6	AR001551
	105	22	100.0	38	6	AR001550
	106	22	100.0	39	6	AR001549
c	107	22	100.0	39	6	AR001562
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	110	22	100.0	40	6	AR001548
	111	22	100.0	41	6	AR001547
c	112	22	100.0	41	6	I72638
	113	22	100.0	42	6	AR001546
	114	22	100.0	43	6	AR001545
	115	22	100.0	45	6	AR001540
	116	22	100.0	45	6	AR001543
c	117	22	100.0	46	6	I45570
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c	123	22	100.0	58	6	I72640
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	125	22	100.0	70	6	I30363
c	126	22	100.0	70	6	I72637
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	128	21	95.5	21	6	AX203700
	129	21	95.5	[redacted]		
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	133	20	90.9	33	6	AR001558
	134	20	90.9	39	6	AR001557
	135	20	90.9	45	6	AR001556
c	136	19.4	88.2	22	6	AR140320
	137	19.4	88.2	22	6	AR206326
	138	19	86.4	20	6	A27240

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I58793 Sequence 8
I58794 Sequence 9
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I49133 Sequence 7
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AR206325 Sequence
AR170398 Sequence
AR001558 Sequence
AR001557 Sequence
AR001556 Sequence
AR140320 Sequence
AR206326 Sequence
A27240 Antiviral D

	139	19	86.4	20	6	I09442
	140	19	86.4	20	6	I72636
	141	19	86.4	22	6	AX363503
c	142	19	86.4	25	6	I91513
c	143	19	86.4	46	6	AR051892
c	144	19	86.4	46	6	E08866
c	145	19	86.4	46	14	HIVPACK
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	147	18.8	85.5	23	6	AR206327
	148	18.8	85.5	32	6	AX306435
	149	18.8	85.5	43	6	I78658
	150	18.8	85.5	43	6	I78659
	151	18.4	83.6	21	6	AR206343
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c	157	17	77.3	17	6	AX418589
c	158	17	77.3	17	6	I28579
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	163	17	77.3	20	6	AR156286
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	165	17	77.3	31	6	AR026209
c	166	17	77.3	31	6	AR026223
	167	17	77.3	31	6	AR026237
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c	169	17	77.3	31	6	I82899
	170	17	77.3	31	6	I82951
c	171	17	77.3	31	6	I82965
	172	17	77.3	31	6	I82979
	173	16.8	76.4	21	6	AR206344
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c	175	16.8	76.4	25	6	AR202366
	176	16.4	74.5	39	6	AR030568
c	177	16.4	74.5	62	6	AR064475
c	178	16	72.7	19	6	I78667
	179	16	72.7	24	6	AR064542
	180	16	72.7	24	6	I65630
	181	16	72.7	43	6	AR001544
c	182	16	72.7	57	6	AR030565
	183	15.8	71.8	24	6	I78660
	184	15.8	71.8	43	6	AX210240
	185	15.6	70.9	43	6	I78649
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	187	15.6	70.9	43	6	I78651
	188	15.6	70.9	43	6	I78652
	189	15.6	70.9	43	6	I78656
	190	15.6	70.9	43	6	I78657
	191	15.4	70.0	20	6	AR100320
	192	15.4	70.0	20	6	AR149975
	193	15.4	70.0	50	6	AR064461
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	196	15	68.2	30	6	AR001542
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	199	14.8	67.3	26	6	I79834
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	201	14.6	66.4	44	6	AR156322
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c	204	14.6	66.4	91	8	AF006068
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	207	14.2	64.5	19	6	AR206333
	208	14.2	64.5	21	6	AR028658
	209	14.2	64.5	21	6	AR053751
	210	14.2	64.5	21	6	AR146251
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E08866 cDNA encodi
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AX306435 Sequence
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A03726 reverse com
A31890 Synthetic M
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AR116258 Sequence
AR156286 Sequence
AR026157 Sequence
AR026209 Sequence
AR026223 Sequence
AR026237 Sequence
E61333 Probe for d
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I82965 Sequence 67
I82979 Sequence 81
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AR055074 Sequence
AR156323 Sequence
AF006068 Fraxinus
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AR206333 Sequence
AR028658 Sequence
AR053751 Sequence
AR146251 Sequence
AR178205 Sequence

	212	14.2	64.5	21	6	I73330 I73330 Sequence 26
	213	14.2	64.5	24	6	I78655 I78655 Sequence 10
c	214	14.2	64.5	25	6	AR030182 AR030182 Sequence
c	215	14.2	64.5	25	6	I17357 I17357 Sequence 7
c	216	14.2	64.5	29	6	AX461477 AX461477 Sequence
	217	14	63.6	18	6	AR043090 AR043090 Sequence
	218	14	63.6	18	6	AR098575 AR098575 Sequence
	219	14	63.6	22	6	AX060328 AX060328 Sequence
	220	14	63.6	36	6	AR036340 AR036340 Sequence
	221	14	63.6	36	6	I72088 I72088 Sequence 3
	222	14	63.6	39	6	AR001559 AR001559 Sequence
	223	14	63.6	43	6	I78646 I78646 Sequence 1
	224	14	63.6	43	6	I78647 I78647 Sequence 2
	225	14	63.6	43	6	I78648 I78648 Sequence 3
c	226	14	63.6	53	6	AR098682 AR098682 Sequence
	227	14	63.6	53	6	AR098683 AR098683 Sequence
c	228	14	63.6	53	6	AR204756 AR204756 Sequence
	229	14	63.6	53	6	AR204757 AR204757 Sequence
c	230	14	63.6	69	6	AX283688 AX283688 Sequence
	231	14	63.6	71	6	AR012490 AR012490 Sequence
	232	14	63.6	71	6	AR020318 AR020318 Sequence
	233	14	63.6	71	6	AR109339 AR109339 Sequence
	234	14	63.6	71	6	I82664 I82664 Sequence 10
	235	14	63.6	72	5	AF420582 AF420582 Salmo sal
c	236	14	63.6	80	11	HSOX6R Z30413 H.sapiens (
c	237	14	63.6	91	14	AY047262S2 AY047263 HIV-1 TV0
c	238	13.8	62.7	51	9	S78662 S78662 Homo sapien
	239	13.8	62.7	97	9	AF010484 AF010484 Homo sapi
c	240	13.6	61.8	21	6	BD012580 BD012580 Human cyt
c	241	13.6	61.8	21	23	BD008148 Bd008148 Human cyt
	242	13.6	61.8	37	6	AR079383 AR079383 Sequence
c	243	13.6	61.8	80	3	AF127338 AF127338 Euprymna
c	244	13.6	61.8	84	3	AF318495 AF318495 Scutigere
c	245	13.6	61.8	94	4	MME309054 AJ309054 Meles mel
	246	13.4	60.9	69	11	AL823984 AL823984 Arabidops
	247	13.4	60.9	73	6	AR012430 AR012430 Sequence
	248	13.4	60.9	73	6	AR020258 AR020258 Sequence
	249	13.4	60.9	73	6	AR109279 AR109279 Sequence
	250	13.4	60.9	73	6	I82604 I82604 Sequence 45
c	251	13.4	60.9	82	11	HUMSWX1496 L47634 Human chrom
	252	13.4	60.9	100	3	AF411993 AF411993 Formica e
	253	13.2	60.0	24	6	A41490 A41490 Sequence 5
	254	13.2	60.0	50	6	AX158892 AX158892 Sequence
c	255	13.2	60.0	50	8	AF247740S1 AF247740 Zea mays
c	256	13.2	60.0	51	6	AX162063 AX162063 Sequence
c	257	13.2	60.0	71	9	HSU38ASNR X97582 H.sapiens s
	258	13.2	60.0	88	6	E05713 E05713 Black pine
	259	13.2	60.0	88	8	MPOCPTRSA M20964 Liverwort c
	260	13.2	60.0	96	6	E00720 E00720 Synthetic D
	261	13.2	60.0	99	6	E01004 E01004 DNA sequenc
	262	13.2	60.0	99	6	E01047 E01047 DNA encodin
	263	13.2	60.0	99	6	E01048 E01048 DNA encodin
	264	13.2	60.0	100	6	AR101829 AR101829 Sequence
c	265	13	59.1	13	6	AR018132 AR018132 Sequence
c	266	13	59.1	13	6	AR018133 AR018133 Sequence
	267	13	59.1	13	6	AR018134 AR018134 Sequence
	268	13	59.1	13	6	AR064541 AR064541 Sequence
	269	13	59.1	13	6	AR206328 AR206328 Sequence
c	270	13	59.1	13	6	I45567 I45567 Sequence 2
	271	13	59.1	20	6	AR100336 AR100336 Sequence
	272	13	59.1	20	6	AR149991 AR149991 Sequence
	273	13	59.1	27	6	AR030170 AR030170 Sequence
c	274	13	59.1	27	6	AR140599 AR140599 Sequence
	275	13	59.1	29	6	AR182585 AR182585 Sequence
	276	13	59.1	30	6	AX148786 AX148786 Sequence
	277	13	59.1	33	6	A45279 A45279 Sequence 10
	278	13	59.1	33	6	A45280 A45280 Sequence 11
	279	13	59.1	33	6	AR116259 AR116259 Sequence
	280	13	59.1	33	6	AR116260 AR116260 Sequence
	281	13	59.1	35	6	AR141975 AR141975 Sequence
	282	13	59.1	35	6	AR202544 AR202544 Sequence
c	283	13	59.1	42	6	AX080391 AX080391 Sequence
	284	13	59.1	51	6	AX203980 AX203980 Sequence
	285	13	59.1	51	6	AX203981 AX203981 Sequence
	286	13	59.1	65	6	AX483292 AX483292 Sequence
c	287	13	59.1	73	6	AX080404 AX080404 Sequence
	288	13	59.1	73	9	AB032820 AB032820 Homo sapi
	289	13	59.1	78	10	S69304S5 S69227 p53 (intron
c	290	13	59.1	88	5	AF372550S1 AF372550 Gallinula
c	291	13	59.1	100	11	G43460 G43460 WIAF-2192-S
	292	12.8	58.2	16	6	AR206331 AR206331 Sequence
	293	12.8	58.2	17	6	AR206332 AR206332 Sequence
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c	295	12.8	58.2	19	6	I78664 I78664 Sequence 19
c	296	12.8	58.2	19	6	I78666 I78666 Sequence 21
c	297	12.8	58.2	20	6	AX298392 AX298392 Sequence
c	298	12.8	58.2	23	6	AR142933 AR142933 Sequence
	299	12.8	58.2	34	6	AX040099 AX040099 Sequence
	300	12.8	58.2	45	6	I09495 I09495 Sequence 13
	301	12.8	58.2	49	6	AX279639 AX279639 Sequence
	302	12.8	58.2	51	6	AX204255 AX204255 Sequence
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	304	12.8	58.2	87	5	AF033554 AF033554 Phyllosco
c	305	12.8	58.2	97	17	HSMC44B11 X88050 H.sapiens D
	306	12.6	57.3	19	6	AR030024 AR030024 Sequence
	307	12.6	57.3	24	6	AX487607 AX487607 Sequence
c	308	12.6	57.3	26	6	AR140606 AR140606 Sequence
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	313	12.6	57.3	32	6	AX356241 AX356241 Sequence
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c	321	12.6	57.3	46	12	SYNPRWF M94408 Artificial
	322	12.6	57.3	50	6	AR032985 AR032985 Sequence
	323	12.6	57.3	50	6	AR209649 AR209649 Sequence
	324	12.6	57.3	50	6	I29725 I29725 Sequence 59
	325	12.6	57.3	50	6	I91399 I91399 Sequence 59
c	326	12.6	57.3	51	6	AX117177 AX117177 Sequence
c	327	12.6	57.3	51	6	AX160433 AX160433 Sequence
	328	12.6	57.3	51	6	AX160986 AX160986 Sequence
	329	12.6	57.3	51	6	AX199439 AX199439 Sequence
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	332	12.6	57.3	60	6	AR011228 AR011228 Sequence
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	334	12.6	57.3	63	6	A18237 A18237 HBV S1 (adw
	335	12.6	57.3	63	6	BD004821 BD004821 Compositi
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c	338	12.6	57.3	71	6	AR054796 AR054796 Sequence
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	343	12.6	57.3	88	8	MPOCPTRSC M20966 Liverwort c
	344	12.6	57.3	96	8	AF317968 AF317968 Arabidops
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c	347	12.4	56.4	27	6	AR197555 AR197555 Sequence
	348	12.4	56.4	30	6	AX050289 AX050289 Sequence
	349	12.4	56.4	30	6	AX474209 AX474209 Sequence
	350	12.4	56.4	31	6	E14828 E14828 PCR primer
c	351	12.4	56.4	35	6	E17165 E17165 Primer. 7/1
	352	12.4	56.4	41	6	AR200829 AR200829 Sequence
c	353	12.4	56.4	41	6	AX040137 AX040137 Sequence
c	354	12.4	56.4	43	6	AR200693 AR200693 Sequence
c	355	12.4	56.4	48	6	A17170 A17170 Oligonucleo
c	356	12.4	56.4	48	6	AR027553 AR027553 Sequence
c	357	12.4	56.4	50	9	S47176S1 S47176 lipoprotein

c 358	12.4	56.4	51	6	AX165573	AX165573 Sequence
359	12.4	56.4	54	6	AX074089	AX074089 Sequence
360	12.4	56.4	54	6	AX074132	AX074132 Sequence
361	12.4	56.4	55	6	AX397798	AX397798 Sequence
362	12.4	56.4	57	6	E15743	E15743 Primer for
363	12.4	56.4	57	9	S57598	S57598 T-cell-rece
364	12.4	56.4	63	9	S57600	S57600 T-cell-rece
365	12.4	56.4	63	9	S57602	S57602 Homo sapien
c 366	12.4	56.4	65	6	AX485443	AX485443 Sequence
367	12.4	56.4	69	6	AR012521	AR012521 Sequence
368	12.4	56.4	69	6	AR020349	AR020349 Sequence
369	12.4	56.4	69	6	AR109370	AR109370 Sequence
370	12.4	56.4	69	6	I82695	I82695 Sequence 13
c 371	12.4	56.4	71	10	MMU403546	AJ403546 M.musculu
372	12.4	56.4	72	10	MMU79537	U79537 Mus musculu
373	12.4	56.4	75	9	HSA305429	AJ305429 Homo sapi
374	12.4	56.4	75	10	AF096407	AF096407 Mus muscu
375	12.4	56.4	78	9	HSA305430	AJ305430 Homo sapi
376	12.4	56.4	84	10	RNU20303	U20303 Rattus norv
377	12.4	56.4	84	10	MMZ86015	Z86015 M.musculus
378	12.4	56.4	84	11	AL773196	AL773196 Arabidops
379	12.4	56.4	84	11	AL773197	AL773197 Arabidops
380	12.4	56.4	85	9	AY006234	AY006234 Homo sapi
381	12.4	56.4	86	10	MMZ86016	Z86016 M.musculus
382	12.4	56.4	87	9	AY006232	AY006232 Homo sapi
383	12.4	56.4	90	9	AY006227	AY006227 Homo sapi
384	12.4	56.4	90	9	AY006228	AY006228 Homo sapi
385	12.4	56.4	90	9	AY006233	AY006233 Homo sapi
386	12.4	56.4	90	9	AY006302	AY006302 Homo sapi
387	12.4	56.4	90	9	HSA405800	AJ405800 Homo sapi
388	12.4	56.4	91	9	AY006110	AY006110 Homo sapi
389	12.4	56.4	91	9	AY006230	AY006230 Homo sapi
c 390	12.4	56.4	91	10	AY041821	AY041821 Oryzomys
c 391	12.4	56.4	91	14	AY047264S2	AY047265 HIV-1 TV0
c 392	12.4	56.4	91	14	AY047268S2	AY047269 HIV-1 TV0
c 393	12.4	56.4	91	14	AY047272S2	AY047273 HIV-1 TV0
c 394	12.4	56.4	91	14	AY047282S2	AY047283 HIV-1 TV0
c 395	12.4	56.4	91	14	AY047284S2	AY047285 HIV-1 TV0
396	12.4	56.4	92	9	AY006236	AY006236 Homo sapi
397	12.4	56.4	93	9	AY006224	AY006224 Homo sapi
398	12.4	56.4	93	9	AY006305	AY006305 Homo sapi
399	12.4	56.4	94	9	AY006226	AY006226 Homo sapi
400	12.4	56.4	94	9	AY006231	AY006231 Homo sapi
401	12.4	56.4	94	9	AY006235	AY006235 Homo sapi
402	12.4	56.4	94	9	AY006304	AY006304 Homo sapi
403	12.4	56.4	95	3	AF299136	AF299136 Evechinus
404	12.4	56.4	95	10	MMV8IN24	Z12545 M.musculus
405	12.4	56.4	95	10	MMV8IN38	Z12550 M.musculus
406	12.4	56.4	96	9	AY006107	AY006107 Homo sapi
c 407	12.4	56.4	97	3	AF454676	AF454676 Lasioglos
408	12.4	56.4	97	9	AY006223	AY006223 Homo sapi
409	12.4	56.4	97	9	AY006229	AY006229 Homo sapi
410	12.4	56.4	97	9	AY006299	AY006299 Homo sapi
411	12.4	56.4	97	10	MMZ86014	Z86014 M.musculus
412	12.4	56.4	98	10	MMV8LK35	Z12544 M.musculus
413	12.4	56.4	98	10	MMV8IN26	Z12546 M.musculus
414	12.4	56.4	98	10	MMV8IN28	Z12547 M.musculus
c 415	12.4	56.4	98	10	MMV8INM5	Z12557 M.musculus
416	12.4	56.4	100	9	AY006225	AY006225 Homo sapi
417	12.4	56.4	100	9	AY006300	AY006300 Homo sapi
418	12.4	56.4	100	14	NCRNAPBS3	Y13708 Human Norwa
419	12.2	55.5	18	6	AR029833	AR029833 Sequence
c 420	12.2	55.5	20	6	AX453152	AX453152 Sequence
421	12.2	55.5	20	6	E15161	E15161 Phosphoroth
c 422	12.2	55.5	20	6	E22407	E22407 Antisense n
c 423	12.2	55.5	20	6	E22408	E22408 Antisense n
c 424	12.2	55.5	21	6	AX099799	AX099799 Sequence
425	12.2	55.5	23	6	BD008043	BD008043 Method of
426	12.2	55.5	24	6	AR092019	AR092019 Sequence
427	12.2	55.5	24	6	AR112154	AR112154 Sequence
428	12.2	55.5	24	6	AR149196	AR149196 Sequence
c 429	12.2	55.5	24	6	AR173215	AR173215 Sequence
c 430	12.2	55.5	25	6	AR090958	AR090958 Sequence
c 431	12.2	55.5	25	6	AR197993	AR197993 Sequence
c 432	12.2	55.5	27	6	AX003574	AX003574 Sequence
c 433	12.2	55.5	27	6	AX299886	AX299886 Sequence
434	12.2	55.5	31	6	AX248885	AX248885 Sequence
435	12.2	55.5	31	6	E05015	E05015 Primer. 9/1
436	12.2	55.5	33	6	AX128309	AX128309 Sequence
437	12.2	55.5	38	6	AX060471	AX060471 Sequence
438	12.2	55.5	40	6	AR095496	AR095496 Sequence
439	12.2	55.5	40	6	AX057070	AX057070 Sequence
c 440	12.2	55.5	50	6	AX164811	AX164811 Sequence
441	12.2	55.5	51	6	AX116761	AX116761 Sequence
c 442	12.2	55.5	51	6	AX160434	AX160434 Sequence
c 443	12.2	55.5	51	6	AX162677	AX162677 Sequence
c 444	12.2	55.5	51	6	E22400	E22400 Antisense n
c 445	12.2	55.5	65	6	AR097770	AR097770 Sequence
c 446	12.2	55.5	65	6	AX483227	AX483227 Sequence
447	12.2	55.5	65	6	AX485312	AX485312 Sequence
c 448	12.2	55.5	71	6	AR054777	AR054777 Sequence
c 449	12.2	55.5	71	6	AR066042	AR066042 Sequence
450	12.2	55.5	72	9	S60877	S60877 LCK-protein
451	12.2	55.5	73	9	S60869	S60869 TCRB (t(1;7
c 452	12.2	55.5	77	6	AR009156	AR009156 Sequence
c 453	12.2	55.5	77	6	I32422	I32422 Sequence 4
454	12.2	55.5	81	5	AF033555	AF033555 Fringilla
c 455	12.2	55.5	83	9	S63933	S63933 IgH (CDR3 r
c 456	12.2	55.5	90	12	SYNPRWH	M94410 Artificial
c 457	12.2	55.5	91	10	MUSAQP1S03	L41514 Mus musculu
458	12	54.5	12	6	AR206322	AR206322 Sequence
459	12	54.5	12	6	AR206323	AR206323 Sequence
460	12	54.5	12	6	AR206324	AR206324 Sequence
461	12	54.5	15	6	AR206329	AR206329 Sequence
462	12	54.5	15	6	AR206330	AR206330 Sequence
c 463	12	54.5	20	6	AR099520	AR099520 Sequence
c 464	12	54.5	20	6	AR178801	AR178801 Sequence
465	12	54.5	21	6	AR006861	AR006861 Sequence
466	12	54.5	21	6	AR080899	AR080899 Sequence
467	12	54.5	21	6	AR173729	AR173729 Sequence
468	12	54.5	22	6	AX074088	AX074088 Sequence
469	12	54.5	22	6	AX074144	AX074144 Sequence
c 470	12	54.5	22	6	AX116474	AX116474 Sequence
c 471	12	54.5	22	6	AX418160	AX418160 Sequence
472	12	54.5	23	6	I12716	I12716 Sequence 14
473	12	54.5	24	6	AX291073	AX291073 Sequence
474	12	54.5	24	6	AX291082	AX291082 Sequence
475	12	54.5	24	6	AX392029	AX392029 Sequence
476	12	54.5	27	6	AX067979	AX067979 Sequence
477	12	54.5	27	6	I42618	I42618 Sequence 8
478	12	54.5	27	6	I42665	I42665 Sequence 55
c 479	12	54.5	28	6	AR157617	AR157617 Sequence
c 480	12	54.5	28	6	AR178564	AR178564 Sequence
481	12	54.5	28	6	I42617	I42617 Sequence 7
482	12	54.5	28	6	I42664	I42664 Sequence 54
c 483	12	54.5	35	6	AR001398	AR001398 Sequence
c 484	12	54.5	35	6	AR078378	AR078378 Sequence
c 485	12	54.5	35	6	AR085229	AR085229 Sequence
c 486	12	54.5	35	6	AR138149	AR138149 Sequence
c 487	12	54.5	35	6	AR194276	AR194276 Sequence
488	12	54.5	37	6	AR006854	AR006854 Sequence
489	12	54.5	37	6	AR080892	AR080892 Sequence
c 490	12	54.5	37	6	AR119930	AR119930 Sequence
491	12	54.5	37	6	AR173722	AR173722 Sequence
c 492	12	54.5	38	6	AX424524	AX424524 Sequence
c 493	12	54.5	39	6	AR051682	AR051682 Sequence
494	12	54.5	40	6	AR030569	AR030569 Sequence
c 495	12	54.5	40	6	AX456400	AX456400 Sequence
c 496	12	54.5	45	6	AR080900	AR080900 Sequence
c 497	12	54.5	45	6	AR173730	AR173730 Sequence
498	12	54.5	46	6	AR032675	AR032675 Sequence
499	12	54.5	46	6	AR209339	AR209339 Sequence
500	12	54.5	46	6	I29415	I29415 Sequence 28
501	12	54.5	46	6	I91089	I91089 Sequence 28
502	12	54.5	47	6	AR121449	AR121449 Sequence
c 503	12	54.5	47	6	AR121450	AR121450 Sequence

c	504	12	54.5	47	6	AX195002 AX195002 Sequence
	505	12	54.5	47	6	I56041 I56041 Sequence 22
c	506	12	54.5	47	6	I56042 I56042 Sequence 23
	507	12	54.5	47	6	I95912 I95912 Sequence 22
c	508	12	54.5	47	6	I95913 I95913 Sequence 23
	509	12	54.5	50	6	AR032859 AR032859 Sequence
	510	12	54.5	50	6	AR209523 AR209523 Sequence
	511	12	54.5	50	6	I29599 I29599 Sequence 47
	512	12	54.5	50	6	I91273 I91273 Sequence 47
c	513	12	54.5	51	6	AX156929 AX156929 Sequence
c	514	12	54.5	51	6	AX156930 AX156930 Sequence
	515	12	54.5	51	6	AX158531 AX158531 Sequence
	516	12	54.5	52	6	AR122336 AR122336 Sequence
c	517	12	54.5	60	6	AR160234 AR160234 Sequence
	518	12	54.5	60	6	AR160239 AR160239 Sequence
	519	12	54.5	60	8	S44200 S44200 class VI zy
	520	12	54.5	61	6	AR118282 AR118282 Sequence
c	521	12	54.5	62	10	AF265758 AF265758 Mus muscu
	522	12	54.5	64	9	S81084S20 S81066 glucose pho
c	523	12	54.5	65	6	AX484190 AX484190 Sequence
	524	12	54.5	65	6	AX486197 AX486197 Sequence
	525	12	54.5	70	6	AR012474 AR012474 Sequence
	526	12	54.5	70	6	AR020302 AR020302 Sequence
	527	12	54.5	70	6	AR109323 AR109323 Sequence
	528	12	54.5	70	6	I82648 I82648 Sequence 89
c	529	12	54.5	76	6	AR042693 AR042693 Sequence
c	530	12	54.5	76	6	AR064826 AR064826 Sequence
c	531	12	54.5	79	4	PCU46759 U46759 Physeter ca
	532	12	54.5	80	6	AR110376 AR110376 Sequence
	533	12	54.5	80	6	BD009396 BD009396 Chimeric,
c	534	12	54.5	81	3	AF015945 AF015945 Carcinus
c	535	12	54.5	81	3	AF144884 AF144884 Priapulus
c	536	12	54.5	81	6	AR096176 AR096176 Sequence
c	537	12	54.5	81	6	AR210575 AR210575 Sequence
	538	12	54.5	81	9	HSU07136 U07136 Human clone
	539	12	54.5	81	14	D87756 D87756 Hepatitis C
	540	12	54.5	81	14	HPC1090C1I D43652 Hepatitis C
c	541	12	54.5	82	11	HUMUT789B L31202 Human STS U
c	542	12	54.5	87	3	PFE272193 AJ272193 Pachymeri
	543	12	54.5	87	6	A42839 A42839 Sequence 17
	544	12	54.5	87	6	I87345 I87345 Sequence 17
	545	12	54.5	87	14	AF050506 AF050506 Human end
	546	12	54.5	87	14	AF050515 AF050515 Human end
	547	12	54.5	88	6	A42834 A42834 Sequence 16
	548	12	54.5	88	6	I87340 I87340 Sequence 16
c	549	12	54.5	89	9	S63934 S63934 IgH (CDR3 r
	550	12	54.5	90	5	AF087830 AF087830 Gallus ga
	551	12	54.5	90	6	A42845 A42845 Sequence 17
	552	12	54.5	90	6	I87351 I87351 Sequence 17
c	553	12	54.5	91	14	AB034436 AB034436 Human imm
c	554	12	54.5	91	14	AB034443 AB034443 Human imm
	555	12	54.5	93	6	A42846 A42846 Sequence 17
	556	12	54.5	93	6	I87352 I87352 Sequence 17
c	557	12	54.5	99	6	I65773 I65773 Sequence 9
	558	12	54.5	99	10	MUSAQP1S04 L41515 Mus musculu
	559	12	54.5	100	10	MMDNDS21 X55239 M.musculus
	560	12	54.5	100	11	HSPF11F3 Z94550 H.sapiens f
	561	11.8	53.6	18	6	AR098354 AR098354 Sequence
	562	11.8	53.6	18	6	AR174188 AR174188 Sequence
	563	11.8	53.6	19	6	AR202163 AR202163 Sequence
c	564	11.8	53.6	21	6	AR198750 AR198750 Sequence
c	565	11.8	53.6	21	6	AX117559 AX117559 Sequence
c	566	11.8	53.6	24	6	AX288614 AX288614 Sequence
c	567	11.8	53.6	25	6	A99250 A99250 Sequence 26
	568	11.8	53.6	30	6	AR118765 AR118765 Sequence
	569	11.8	53.6	30	6	I06397 I06397 Sequence 17
	570	11.8	53.6	30	6	I32178 I32178 Sequence 54
	571	11.8	53.6	30	6	I34269 I34269 Sequence 54
	572	11.8	53.6	30	6	I82474 I82474 Sequence 54
c	573	11.8	53.6	31	6	AX107904 AX107904 Sequence
c	574	11.8	53.6	31	6	AX248858 AX248858 Sequence
c	575	11.8	53.6	31	6	AX249138 AX249138 Sequence
	576	11.8	53.6	33	6	AX151706 AX151706 Sequence
	577	11.8	53.6	36	10	MMU299486 AJ299486 Mus muscu
c	578	11.8	53.6	40	6	AR064974 AR064974 Sequence
	579	11.8	53.6	60	6	AR177471 AR177471 Sequence
c	580	11.8	53.6	60	6	AR177472 AR177472 Sequence
c	581	11.8	53.6	63	3	HMU09802 U09802 Herdmania m
c	582	11.8	53.6	65	1	S74675S2 S74677 16S rRNA (V
c	583	11.8	53.6	72	9	HUMIGBLYMC M87023 Human immun
c	584	11.8	53.6	75	9	S63942 S63942 IgH (CDR3 r
	585	11.8	53.6	76	8	NEUMTTRV K00149 Neurospora
c	586	11.8	53.6	80	9	S57152 S57152 Homo sapien
c	587	11.8	53.6	81	3	AF015943 AF015943 Ulophysem
	588	11.8	53.6	81	14	AF207080 AF207080 Hepatitis
	589	11.8	53.6	81	14	AF207081 AF207081 Hepatitis
	590	11.8	53.6	81	14	AF207082 AF207082 Hepatitis
	591	11.8	53.6	81	14	AF207083 AF207083 Hepatitis
	592	11.8	53.6	81	14	AF207084 AF207084 Hepatitis
	593	11.8	53.6	81	14	AF207085 AF207085 Hepatitis
	594	11.8	53.6	81	14	AF207086 AF207086 Hepatitis
	595	11.8	53.6	81	14	AF207087 AF207087 Hepatitis
	596	11.8	53.6	81	14	AF207088 AF207088 Hepatitis
	597	11.8	53.6	81	14	AF207089 AF207089 Hepatitis
	598	11.8	53.6	81	14	AF207090 AF207090 Hepatitis
	599	11.8	53.6	81	14	AF207091 AF207091 Hepatitis
	600	11.8	53.6	81	14	AF207092 AF207092 Hepatitis
	601	11.8	53.6	81	14	AF207093 AF207093 Hepatitis
	602	11.8	53.6	81	14	AF207095 AF207095 Hepatitis
	603	11.8	53.6	81	14	AF207096 AF207096 Hepatitis
	604	11.8	53.6	81	14	AF207097 AF207097 Hepatitis
	605	11.8	53.6	81	14	AF207098 AF207098 Hepatitis
	606	11.8	53.6	81	14	AF207099 AF207099 Hepatitis
c	607	11.8	53.6	82	3	AF020959 AF020959 Nematoste
c	608	11.8	53.6	83	10	MMVIMV30 X89147 M.musculus
c	609	11.8	53.6	88	9	U00823 U00823 Human "beta-
	610	11.8	53.6	92	9	HUMPK30 D28371 Human mRNA
c	611	11.8	53.6	94	6	AX387879 AX387879 Sequence
	612	11.8	53.6	100	9	HUMLDH27 D28368 Human mRNA
c	613	11.6	52.7	18	6	AX317621 AX317621 Sequence
	614	11.6	52.7	20	6	AR037341 AR037341 Sequence
	615	11.6	52.7	20	6	AR040624 AR040624 Sequence
	616	11.6	52.7	20	6	E11009 E11009 Primer for
	617	11.6	52.7	20	6	I19635 I19635 Sequence 16
	618	11.6	52.7	20	6	I88645 I88645 Sequence 27
	619	11.6	52.7	21	6	AX191810 AX191810 Sequence
c	620	11.6	52.7	22	9	HS3CF71L X87712 H.sapiens p
c	621	11.6	52.7	24	6	AX397670 AX397670 Sequence
	622	11.6	52.7	24	6	AX458684 AX458684 Sequence
c	623	11.6	52.7	25	6	A65298 A65298 Sequence 21
c	624	11.6	52.7	25	6	AR150446 AR150446 Sequence
	625	11.6	52.7	25	6	AX317618 AX317618 Sequence
c	626	11.6	52.7	25	11	C75924 C75924 Homo sapien
c	627	11.6	52.7	26	6	A65299 A65299 Sequence 22
c	628	11.6	52.7	26	6	AR150447 AR150447 Sequence
	629	11.6	52.7	26	6	AR211783 AR211783 Sequence
	630	11.6	52.7	26	6	BD009910 BD009910 Compositi
	631	11.6	52.7	27	6	AX090069 AX090069 Sequence
c	632	11.6	52.7	29	6	AR039142 AR039142 Sequence
c	633	11.6	52.7	29	6	AR065272 AR065272 Sequence
c	634	11.6	52.7	33	6	AX115955 AX115955 Sequence
c	635	11.6	52.7	34	6	A92573 A92573 Sequence 3
c	636	11.6	52.7	34	6	AR212248 AR212248 Sequence
c	637	11.6	52.7	34	6	BD003669 BD003669 Utilizati
c	638	11.6	52.7	40	6	AR135225 AR135225 Sequence
c	639	11.6	52.7	40	6	AR146721 AR146721 Sequence
c	640	11.6	52.7	40	6	AR152292 AR152292 Sequence
c	641	11.6	52.7	40	6	AR157830 AR157830 Sequence
	642	11.6	52.7	40	6	AX456445 AX456445 Sequence
	643	11.6	52.7	42	6	AR141022 AR141022 Sequence
c	644	11.6	52.7	43	6	AX207948 AX207948 Sequence
	645	11.6	52.7	43	6	AX207950 AX207950 Sequence
	646	11.6	52.7	43	6	AX466471 AX466471 Sequence
c	647	11.6	52.7	47	6	AX194951 AX194951 Sequence
c	648	11.6	52.7	47	12	SYNPRWA M94403 Artificial
	649	11.6	52.7	48	6	A93514 A93514 Sequence 7

c 650	11.6	52.7	48	6	I23498	I23498 Sequence 3
651	11.6	52.7	50	6	AX165840	AX165840 Sequence
c 652	11.6	52.7	50	6	AX199420	AX199420 Sequence
c 653	11.6	52.7	50	6	AX199422	AX199422 Sequence
c 654	11.6	52.7	51	6	AX157005	AX157005 Sequence
c 655	11.6	52.7	51	6	AX157006	AX157006 Sequence
656	11.6	52.7	51	6	AX157609	AX157609 Sequence
c 657	11.6	52.7	51	6	AX199419	AX199419 Sequence
c 658	11.6	52.7	51	6	AX199421	AX199421 Sequence
c 659	11.6	52.7	51	6	AX204239	AX204239 Sequence
c 660	11.6	52.7	51	6	AX204348	AX204348 Sequence
661	11.6	52.7	55	9	HSD3SS	X66228 H.sapiens d
662	11.6	52.7	57	6	AR199607	AR199607 Sequence
663	11.6	52.7	57	6	AX366870	AX366870 Sequence
c 664	11.6	52.7	62	6	AX148745	AX148745 Sequence
665	11.6	52.7	62	10	RATIVS303	M91241 Rat L-type
666	11.6	52.7	65	6	AX482855	AX482855 Sequence
c 667	11.6	52.7	66	9	HSVAVPOG19	AF030219 Homo sapi
c 668	11.6	52.7	67	6	A36470	A36470 Sequence 11
c 669	11.6	52.7	67	6	AR071656	AR071656 Sequence
c 670	11.6	52.7	67	6	AR080103	AR080103 Sequence
c 671	11.6	52.7	67	6	AR202436	AR202436 Sequence
c 672	11.6	52.7	70	6	I72523	I72523 Sequence 10
c 673	11.6	52.7	76	5	AF051705	AF051705 Centrocer
c 674	11.6	52.7	76	5	AF051725	AF051725 Cecropis
c 675	11.6	52.7	76	9	S64495	S64495 IgH (CDR3 r
c 676	11.6	52.7	78	5	AF051706	AF051706 Centrocer
c 677	11.6	52.7	80	3	AF011277	AF011277 Acanthoka
678	11.6	52.7	80	9	HSPA5E10	Z79362 H.sapiens f
c 679	11.6	52.7	81	3	AY096249	AY096249 Haloclava
c 680	11.6	52.7	81	5	GGIGACR5	AF190137 Gallus ga
c 681	11.6	52.7	82	5	AF051712	AF051712 Pyrrhula
c 682	11.6	52.7	82	5	AF051722	AF051722 Progne ch
683	11.6	52.7	82	6	AX195313	AX195313 Sequence
c 684	11.6	52.7	84	5	AF051713	AF051713 Campylorh
c 685	11.6	52.7	84	5	AF051714	AF051714 Campylorh
c 686	11.6	52.7	84	5	AF051715	AF051715 Thryothor
c 687	11.6	52.7	84	5	AF051720	AF051720 Psalidopr
c 688	11.6	52.7	86	5	AF051704	AF051704 Struthio
c 689	11.6	52.7	86	5	AF051711	AF051711 Ficedula
c 690	11.6	52.7	86	5	AF051723	AF051723 Petrochel
c 691	11.6	52.7	86	5	AF051724	AF051724 Cecropis
c 692	11.6	52.7	88	5	AF051718	AF051718 Acrocepha
693	11.6	52.7	88	8	MPOCPTRSB	M20965 Liverwort c
c 694	11.6	52.7	90	3	AF362093	AF362093 Lithobius
c 695	11.6	52.7	90	5	AF051717	AF051717 Acrocepha
696	11.6	52.7	90	6	AX376948	AX376948 Sequence
c 697	11.6	52.7	90	6	E05340	E05340 Listeria mo
698	11.6	52.7	90	10	MMTCRVJAS	Z22845 M.musculus
c 699	11.6	52.7	92	5	AF051719	AF051719 Acrocepha
c 700	11.6	52.7	94	5	AF051710	AF051710 Oceanodro
701	11.6	52.7	94	6	AX440015	AX440015 Sequence
702	11.6	52.7	94	8	VFSN45LR	X04787 Broad bean
c 703	11.6	52.7	95	3	AGXH454	Z72086 A.gambiae s
c 704	11.6	52.7	95	6	AR165689	AR165689 Sequence
c 705	11.6	52.7	96	6	A21832	A21832 Polynucleot
c 706	11.6	52.7	96	6	A39970	A39970 Sequence 3
707	11.6	52.7	96	6	AR200232	AR200232 Sequence
c 708	11.6	52.7	98	6	AR165688	AR165688 Sequence
c 709	11.6	52.7	98	6	I91501	I91501 Sequence 35
710	11.6	52.7	99	10	AF096382	AF096382 Mus muscu
711	11.6	52.7	100	4	AY045524	AY045524 Panthera
712	11.4	51.8	15	6	AR131837	AR131837 Sequence
713	11.4	51.8	17	6	AR176148	AR176148 Sequence
714	11.4	51.8	17	6	AX191184	AX191184 Sequence
c 715	11.4	51.8	18	6	AR105021	AR105021 Sequence
c 716	11.4	51.8	18	6	AX101065	AX101065 Sequence
717	11.4	51.8	18	6	AX101067	AX101067 Sequence
c 718	11.4	51.8	18	9	HSRETP18	X79757 H.sapiens R
c 719	11.4	51.8	20	6	AX293247	AX293247 Sequence
c 720	11.4	51.8	20	6	AX300508	AX300508 Sequence
721	11.4	51.8	20	6	AX300510	AX300510 Sequence
722	11.4	51.8	20	6	AX402163	AX402163 Sequence
c 723	11.4	51.8	20	6	I82530	I82530 Sequence 11
c 724	11.4	51.8	20	6	I93768	I93768 Sequence 11
c 725	11.4	51.8	21	6	AR137433	AR137433 Sequence
c 726	11.4	51.8	21	6	AX097316	AX097316 Sequence
c 727	11.4	51.8	21	6	AX097362	AX097362 Sequence
728	11.4	51.8	21	6	AX137780	AX137780 Sequence
729	11.4	51.8	21	6	AX370582	AX370582 Sequence
730	11.4	51.8	21	6	E54093	E54093 Novel gene
731	11.4	51.8	22	6	AX211675	AX211675 Sequence
c 732	11.4	51.8	22	6	AX427064	AX427064 Sequence
733	11.4	51.8	23	6	A14168	A14168 vectorette
c 734	11.4	51.8	23	6	A45285	A45285 Sequence 16
735	11.4	51.8	23	6	AR099727	AR099727 Sequence
c 736	11.4	51.8	23	6	AR116265	AR116265 Sequence
c 737	11.4	51.8	23	6	AX058583	AX058583 Sequence
c 738	11.4	51.8	23	6	AX254776	AX254776 Sequence
739	11.4	51.8	23	6	AX300515	AX300515 Sequence
c 740	11.4	51.8	23	6	AX427063	AX427063 Sequence
c 741	11.4	51.8	24	6	A22615	A22615 Oligonucleo
c 742	11.4	51.8	24	6	I21805	I21805 Sequence 19
c 743	11.4	51.8	25	6	AX254648	AX254648 Sequence
744	11.4	51.8	26	6	A01116	A01116 SalI-BglII-
c 745	11.4	51.8	26	6	A01117	A01117 SalI-BglII-
c 746	11.4	51.8	26	6	AR001202	AR001202 Sequence
c 747	11.4	51.8	26	6	AX038114	AX038114 Sequence
748	11.4	51.8	26	6	AX038115	AX038115 Sequence
c 749	11.4	51.8	26	6	AX146514	AX146514 Sequence
c 750	11.4	51.8	26	6	E11040	E11040 Oligonucleo
751	11.4	51.8	28	6	A42599	A42599 Sequence 11
752	11.4	51.8	28	6	A88787	A88787 Sequence 93
c 753	11.4	51.8	28	6	AX259883	AX259883 Sequence
c 754	11.4	51.8	28	6	I40140	I40140 Sequence 22
755	11.4	51.8	30	6	A14059	A14059 Nucleotide
c 756	11.4	51.8	30	6	AR028324	AR028324 Sequence
c 757	11.4	51.8	30	6	AR125809	AR125809 Sequence
c 758	11.4	51.8	30	6	AX058695	AX058695 Sequence
c 759	11.4	51.8	30	6	AX074011	AX074011 Sequence
c 760	11.4	51.8	30	6	I47221	I47221 Sequence 15
761	11.4	51.8	31	6	AX248582	AX248582 Sequence
762	11.4	51.8	36	6	AR084536	AR084536 Sequence
c 763	11.4	51.8	36	6	AR084537	AR084537 Sequence
c 764	11.4	51.8	38	6	AR046280	AR046280 Sequence
c 765	11.4	51.8	38	6	I37831	I37831 Sequence 84
c 766	11.4	51.8	38	6	I37974	I37974 Sequence 98
c 767	11.4	51.8	38	6	I53332	I53332 Sequence 10
c 768	11.4	51.8	38	6	I94681	I94681 Sequence 84
c 769	11.4	51.8	38	6	I94824	I94824 Sequence 98
c 770	11.4	51.8	40	6	AR053631	AR053631 Sequence
771	11.4	51.8	40	6	AX080990	AX080990 Sequence
772	11.4	51.8	41	6	AR109085	AR109085 Sequence
773	11.4	51.8	41	6	AR200740	AR200740 Sequence
774	11.4	51.8	42	6	AX060318	AX060318 Sequence
c 775	11.4	51.8	45	6	A26132	A26132 Artificial
c 776	11.4	51.8	45	6	A29559	A29559 K.lactis ge
777	11.4	51.8	45	6	AR009531	AR009531 Sequence
c 778	11.4	51.8	45	6	AR086445	AR086445 Sequence
c 779	11.4	51.8	45	6	AR102218	AR102218 Sequence
780	11.4	51.8	45	6	AR172143	AR172143 Sequence
c 781	11.4	51.8	45	6	I33670	I33670 Sequence 13
c 782	11.4	51.8	45	6	I43818	I43818 Sequence 5
783	11.4	51.8	45	6	I66205	I66205 Sequence 12
784	11.4	51.8	45	6	I66218	I66218 Sequence 12
c 785	11.4	51.8	47	6	AR150542	AR150542 Sequence
786	11.4	51.8	47	6	AX195020	AX195020 Sequence
c 787	11.4	51.8	47	6	BD001828	BD001828 Method fo
c 788	11.4	51.8	47	6	I77232	I77232 Sequence 22
789	11.4	51.8	48	6	A40264	A40264 Sequence 4
790	11.4	51.8	48	6	AR193090	AR193090 Sequence
c 791	11.4	51.8	49	6	AR178012	AR178012 Sequence
c 792	11.4	51.8	49	6	AR178013	AR178013 Sequence
c 793	11.4	51.8	49	6	AX254646	AX254646 Sequence
794	11.4	51.8	49	6	AX328622	AX328622 Sequence
795	11.4	51.8	49	6	BD007505	BD007505 High-dens

796	11.4	51.8	50	6	A45286	A45286 Sequence 17
797	11.4	51.8	50	6	A92283	A92283 Sequence 2
798	11.4	51.8	50	6	A92334	A92334 Sequence 2
799	11.4	51.8	50	6	AR116266	AR116266 Sequence
800	11.4	51.8	50	6	AX156824	AX156824 Sequence
c 801	11.4	51.8	50	6	AX160074	AX160074 Sequence
c 802	11.4	51.8	50	6	AX162064	AX162064 Sequence
803	11.4	51.8	50	6	AX190214	AX190214 Sequence
804	11.4	51.8	50	6	AX204199	AX204199 Sequence
805	11.4	51.8	50	6	BD007224	BD007224 Lentiviru
c 806	11.4	51.8	51	6	AX157737	AX157737 Sequence
c 807	11.4	51.8	51	6	AX157738	AX157738 Sequence
c 808	11.4	51.8	51	6	AX157857	AX157857 Sequence
c 809	11.4	51.8	51	6	AX159061	AX159061 Sequence
c 810	11.4	51.8	51	6	AX160073	AX160073 Sequence
811	11.4	51.8	51	6	AX162233	AX162233 Sequence
c 812	11.4	51.8	51	6	AX162475	AX162475 Sequence
c 813	11.4	51.8	51	6	AX162582	AX162582 Sequence
c 814	11.4	51.8	51	6	AX162718	AX162718 Sequence
815	11.4	51.8	51	6	AX190364	AX190364 Sequence
816	11.4	51.8	51	6	AX190365	AX190365 Sequence
c 817	11.4	51.8	51	6	AX190372	AX190372 Sequence
c 818	11.4	51.8	51	6	AX190373	AX190373 Sequence
819	11.4	51.8	51	6	AX204143	AX204143 Sequence
c 820	11.4	51.8	51	6	AX449473	AX449473 Sequence
821	11.4	51.8	51	9	AB013762	AB013762 Macaca as
822	11.4	51.8	51	9	AB013763	AB013763 Macaca as
823	11.4	51.8	51	9	AB013764	AB013764 Macaca fa
824	11.4	51.8	52	6	A03834	A03834 Artificial
825	11.4	51.8	55	6	I77233	I77233 Sequence 23
c 826	11.4	51.8	56	6	AX256423	AX256423 Sequence
827	11.4	51.8	58	6	AR208349	AR208349 Sequence
828	11.4	51.8	60	9	AB013761	AB013761 Macaca mu
c 829	11.4	51.8	60	14	AF466486	AF466486 Hepatitis
c 830	11.4	51.8	60	14	AF466493	AF466493 Hepatitis
831	11.4	51.8	62	6	A59482	A59482 Sequence 32
832	11.4	51.8	63	3	DME300080	AJ300080 Drosophil
c 833	11.4	51.8	63	17	HSMC48H08	X88001 H.sapiens D
c 834	11.4	51.8	64	11	HUMUT272A	L29950 Human STS U
835	11.4	51.8	65	6	AX482999	AX482999 Sequence
836	11.4	51.8	65	6	AX483162	AX483162 Sequence
c 837	11.4	51.8	65	6	AX485160	AX485160 Sequence
838	11.4	51.8	65	6	AX485504	AX485504 Sequence
c 839	11.4	51.8	66	6	AR002290	AR002290 Sequence
c 840	11.4	51.8	66	6	AR053141	AR053141 Sequence
c 841	11.4	51.8	66	6	AR055670	AR055670 Sequence
842	11.4	51.8	66	6	AX080586	AX080586 Sequence
c 843	11.4	51.8	66	9	AF189382	AF189382 Homo sapi
c 844	11.4	51.8	68	9	HSZ98218	Z98218 H.sapiens D
c 845	11.4	51.8	71	6	AR193222	AR193222 Sequence
846	11.4	51.8	71	12	SYNGAPDH	M74580 Synthetic G
847	11.4	51.8	73	6	AR012429	AR012429 Sequence
848	11.4	51.8	73	6	AR020257	AR020257 Sequence
849	11.4	51.8	73	6	AR109278	AR109278 Sequence
850	11.4	51.8	73	6	I82603	I82603 Sequence 44
851	11.4	51.8	74	12	SYNINSPN2	J02554 Rat insulin
c 852	11.4	51.8	77	6	AX328476	AX328476 Sequence
c 853	11.4	51.8	81	3	AF010173	AF010173 Ethmostig
854	11.4	51.8	81	14	AF148867	AF148867 Norwalk-l
855	11.4	51.8	83	5	TMI250452	AJ250452 Trisopter
856	11.4	51.8	83	6	AX080696	AX080696 Sequence
c 857	11.4	51.8	83	8	AF062783	AF062783 Lupinus a
c 858	11.4	51.8	83	9	S63931	S63931 IgH {CDR3 r
c 859	11.4	51.8	83	9	S63932	S63932 IgH {CDR3 r
c 860	11.4	51.8	83	10	MMU403573	AJ403573 M.musculu
c 861	11.4	51.8	84	5	CHKCOLXIVA	L11658 Chicken alp
c 862	11.4	51.8	84	8	AF062785	AF062785 Trifolium
c 863	11.4	51.8	84	10	AF320076S4	AF320079 Mus muscu
c 864	11.4	51.8	85	11	G44366	G44366 WIAF-4135-S
c 865	11.4	51.8	87	6	AR054875	AR054875 Sequence
c 866	11.4	51.8	87	6	AR054876	AR054876 Sequence
c 867	11.4	51.8	87	6	AR066140	AR066140 Sequence
c 868	11.4	51.8	87	6	AR066141	AR066141 Sequence
c 869	11.4	51.8	87	6	AR105032	AR105032 Sequence
c 870	11.4	51.8	87	8	AF522869	AF522869 Araucaria
c 871	11.4	51.8	88	8	SPO251855	AJ251855 Schizosac
c 872	11.4	51.8	88	9	HSRPTDNAC	Z21984 H.sapiens r
873	11.4	51.8	88	10	RNPTHR88	X95094 R.norvegicu
c 874	11.4	51.8	89	8	AF522868	AF522868 Araucaria
875	11.4	51.8	89	10	MUSCCBF14	M60642 Mouse facto
c 876	11.4	51.8	90	6	AR199542	AR199542 Sequence
c 877	11.4	51.8	90	6	AX239591	AX239591 Sequence
c 878	11.4	51.8	91	8	AF263002	AF263002 Ditylum b
c 879	11.4	51.8	91	10	MMD1NDS1	X55201 M.musculus
c 880	11.4	51.8	91	14	AB034435	AB034435 Human imm
881	11.4	51.8	93	5	AF033553	AF033553 Acrocepha
882	11.4	51.8	93	10	RATNACHRR1	J05232 Rat neurona
c 883	11.4	51.8	95	6	AR165724	AR165724 Sequence
884	11.4	51.8	95	6	AX080700	AX080700 Sequence
885	11.4	51.8	95	9	HSIIPKR10	U50641 Human inter
886	11.4	51.8	95	9	HSSTP2S05	U72200 Human pheno
c 887	11.4	51.8	95	10	F321780S29	AF321808 Mus muscu
c 888	11.4	51.8	95	11	HUMUT5301A	L30827 Human STS U
889	11.4	51.8	96	4	SSU62628	U62628 Sus scrofa
c 890	11.4	51.8	96	5	AF420574	AF420574 Salmo sal
c 891	11.4	51.8	97	6	A45370	A45370 Sequence 40
c 892	11.4	51.8	97	6	AR061175	AR061175 Sequence
c 893	11.4	51.8	97	9	HSU32598	U32598 Human pre-B
c 894	11.4	51.8	97	9	HSWG2H11	X86911 H.sapiens A
895	11.4	51.8	99	6	AX080697	AX080697 Sequence
c 896	11.4	51.8	100	6	AR101829	AR101829 Sequence
897	11.4	51.8	100	6	AR202427	AR202427 Sequence
898	11.4	51.8	100	6	AR202430	AR202430 Sequence
c 899	11.4	51.8	100	11	HSPE52G01	AL033906 H.sapiens
900	11.2	50.9	18	6	AX317690	AX317690 Sequence
c 901	11.2	50.9	19	6	AR035143	AR035143 Sequence
c 902	11.2	50.9	19	6	I78661	I78661 Sequence 16
c 903	11.2	50.9	19	6	I78662	I78662 Sequence 17
c 904	11.2	50.9	20	6	AR070810	AR070810 Sequence
c 905	11.2	50.9	20	6	AR104498	AR104498 Sequence
c 906	11.2	50.9	20	6	E05216	E05216 DNA sequenc
c 907	11.2	50.9	21	6	AR069242	AR069242 Sequence
c 908	11.2	50.9	21	12	AB069390	AB069390 Synthetic
c 909	11.2	50.9	21	12	AB069535	AB069535 Synthetic
910	11.2	50.9	22	6	AX034808	AX034808 Sequence
c 911	11.2	50.9	22	6	AX241135	AX241135 Sequence
912	11.2	50.9	22	6	AX304995	AX304995 Sequence
913	11.2	50.9	22	6	AX306524	AX306524 Sequence
c 914	11.2	50.9	22	6	AX356947	AX356947 Sequence
c 915	11.2	50.9	22	6	AX486725	AX486725 Sequence
c 916	11.2	50.9	23	6	I50817	I50817 Sequence 8
c 917	11.2	50.9	24	6	A25725	A25725 Ck5'FOR pri
c 918	11.2	50.9	24	6	AR016209	AR016209 Sequence
c 919	11.2	50.9	24	6	AR051397	AR051397 Sequence
c 920	11.2	50.9	24	6	AR060243	AR060243 Sequence
c 921	11.2	50.9	24	6	AR060257	AR060257 Sequence
c 922	11.2	50.9	24	6	AR060273	AR060273 Sequence
c 923	11.2	50.9	24	6	AX343776	AX343776 Sequence
c 924	11.2	50.9	25	6	AR037105	AR037105 Sequence
c 925	11.2	50.9	25	6	AR070343	AR070343 Sequence
926	11.2	50.9	25	6	E26697	E26697 Transgenic
c 927	11.2	50.9	26	6	AR061819	AR061819 Sequence
928	11.2	50.9	27	6	AR109691	AR109691 Sequence
c 929	11.2	50.9	27	6	AR185217	AR185217 Sequence
930	11.2	50.9	27	6	AX027367	AX027367 Sequence
931	11.2	50.9	30	6	AR004745	AR004745 Sequence
932	11.2	50.9	30	6	AR008231	AR008231 Sequence
933	11.2	50.9	30	6	AR137014	AR137014 Sequence
934	11.2	50.9	30	6	AX012416	AX012416 Sequence
c 935	11.2	50.9	30	6	AX304637	AX304637 Sequence
936	11.2	50.9	30	6	E51009	E51009 Improved pr
c 937	11.2	50.9	30	6	I29838	I29838 Sequence 24
938	11.2	50.9	30	6	I77015	I77015 Sequence 75
939	11.2	50.9	30	6	I81010	I81010 Sequence 75
940	11.2	50.9	30	6	I81106	I81106 Sequence 75
941	11.2	50.9	31	6	AX006554	AX006554 Sequence

942	11.2	50.9	31	6	AX006658	AX006658 Sequence
943	11.2	50.9	31	6	AX025370	AX025370 Sequence
944	11.2	50.9	31	6	AX030262	AX030262 Sequence
945	11.2	50.9	31	6	AX030333	AX030333 Sequence
946	11.2	50.9	31	6	AX034830	AX034830 Sequence
947	11.2	50.9	31	6	AX076417	AX076417 Sequence
948	11.2	50.9	31	6	AX138179	AX138179 Sequence
949	11.2	50.9	31	6	AX399587	AX399587 Sequence
950	11.2	50.9	31	6	AX399766	AX399766 Sequence
951	11.2	50.9	31	6	AX403943	AX403943 Sequence
952	11.2	50.9	31	6	AX456822	AX456822 Sequence
c 953	11.2	50.9	32	6	AR029677	AR029677 Sequence
c 954	11.2	50.9	32	6	AX281027	AX281027 Sequence
c 955	11.2	50.9	32	6	I26213	I26213 Sequence 2
c 956	11.2	50.9	33	6	AX027366	AX027366 Sequence
c 957	11.2	50.9	33	6	AX128607	AX128607 Sequence
c 958	11.2	50.9	33	6	AX357329	AX357329 Sequence
959	11.2	50.9	34	6	AR145908	AR145908 Sequence
960	11.2	50.9	35	6	AX392103	AX392103 Sequence
c 961	11.2	50.9	35	6	E10812	E10812 Probe for d
c 962	11.2	50.9	36	6	AR021388	AR021388 Sequence
c 963	11.2	50.9	36	6	AR042950	AR042950 Sequence
c 964	11.2	50.9	36	6	AR161258	AR161258 Sequence
c 965	11.2	50.9	36	6	AX356940	AX356940 Sequence
c 966	11.2	50.9	36	6	AX356948	AX356948 Sequence
c 967	11.2	50.9	36	6	I43939	I43939 Sequence 28
c 968	11.2	50.9	36	6	I62941	I62941 Sequence 36
c 969	11.2	50.9	36	6	I88694	I88694 Sequence 36
970	11.2	50.9	37	6	A25167	A25167 oligonucleo
971	11.2	50.9	39	6	AR018083	AR018083 Sequence
972	11.2	50.9	39	6	AR051923	AR051923 Sequence
c 973	11.2	50.9	40	6	AR107145	AR107145 Sequence
c 974	11.2	50.9	40	6	AR161397	AR161397 Sequence
c 975	11.2	50.9	40	6	AR181034	AR181034 Sequence
c 976	11.2	50.9	41	6	AR156421	AR156421 Sequence
977	11.2	50.9	42	6	A04432	A04432 Oligonucleo
c 978	11.2	50.9	42	6	A05094	A05094 Oligonucleo
979	11.2	50.9	42	6	A09579	A09579 Nucleotide
c 980	11.2	50.9	42	6	A93509	A93509 Sequence 2
981	11.2	50.9	42	6	AR021385	AR021385 Sequence
982	11.2	50.9	42	6	AR042947	AR042947 Sequence
c 983	11.2	50.9	42	6	AR100954	AR100954 Sequence
984	11.2	50.9	42	6	AR161255	AR161255 Sequence
985	11.2	50.9	42	6	I43936	I43936 Sequence 25
986	11.2	50.9	42	6	I62938	I62938 Sequence 33
987	11.2	50.9	42	6	I88691	I88691 Sequence 33
c 988	11.2	50.9	44	6	AX157237	AX157237 Sequence
c 989	11.2	50.9	44	6	AX157238	AX157238 Sequence
c 990	11.2	50.9	45	6	A45054	A45054 Sequence 29
c 991	11.2	50.9	45	6	AR029670	AR029670 Sequence
992	11.2	50.9	45	6	AR032519	AR032519 Sequence
993	11.2	50.9	45	6	AR209183	AR209183 Sequence
994	11.2	50.9	45	6	I29259	I29259 Sequence 13
995	11.2	50.9	45	6	I90933	I90933 Sequence 13
c 996	11.2	50.9	45	9	S59765	S59765 IgVH-pre-B-
997	11.2	50.9	46	6	A09563	A09563 Nucleotide
998	11.2	50.9	46	6	A21289	A21289 Nucleotide
999	11.2	50.9	46	6	A31611	A31611 Synthetic P
1000	11.2	50.9	46	6	AR053269	AR053269 Sequence

ALIGNMENTS

```
RESULT 1
I49132
LOCUS       I49132                    22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 6 from patent US 5627277.
ACCESSION   I49132
VERSION     I49132.1  GI:2467595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Cohen,A.S., Bourque,A. and Vilenchik,M.
  TITLE     Method for analyzing oligonucleotide analogs
  JOURNAL   Patent: US 5627277-A 6 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        2 a     11 c      1 g      8 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      1 TCGCACCCATCTCTCTCCTTCT 22


RESULT 2
I49131
LOCUS       I49131                    23 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 5 from patent US 5627277.
ACCESSION   I49131
VERSION     I49131.1  GI:2467594
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Cohen,A.S., Bourque,A. and Vilenchik,M.
  TITLE     Method for analyzing oligonucleotide analogs
  JOURNAL   Patent: US 5627277-A 5 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
BASE COUNT        2 a     12 c      1 g      8 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      2 TCGCACCCATCTCTCTCCTTCT 23


RESULT 3
I49130
LOCUS       I49130                    24 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5627277.
ACCESSION   I49130
VERSION     I49130.1  GI:2467593
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cohen,A.S., Bourque,A. and Vilenchik,M.
  TITLE     Method for analyzing oligonucleotide analogs
  JOURNAL   Patent: US 5627277-A 4 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        2 a     12 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      3 TCGCACCCATCTCTCTCCTTCT 24


RESULT 4
AR001561
LOCUS       AR001561                  25 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 22 from patent US 5739308.
ACCESSION   AR001561
VERSION     AR001561.1  GI:3963628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kandimalla,E.R. and Agrawal,S.
  TITLE     Integrated oligonucleotides
  JOURNAL   Patent: US 5739308-A 22 14-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 5
AR052661
LOCUS       AR052661                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5833944.
ACCESSION   AR052661
VERSION     AR052661.1  GI:5977523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Iyer,R.P., Agrawal,S. and Tan,W.
  TITLE     Procedure for the solid phase synthesis of .sup.35 S-labeled
            oligonucleotides with 3H-1,2-benzodithiol-3-one-1,1-dioxide
  JOURNAL   Patent: US 5833944-A 1 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 6
AR052662
LOCUS       AR052662                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5833944.
ACCESSION   AR052662
VERSION     AR052662.1  GI:5977524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Iyer,R.P., Agrawal,S. and Tan,W.
  TITLE     Procedure for the solid phase synthesis of .sup.35 S-labeled
            oligonucleotides with 3H-1,2-benzodithiol-3-one-1,1-dioxide
  JOURNAL   Patent: US 5833944-A 2 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 7
AR052663
LOCUS       AR052663                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5833944.
ACCESSION   AR052663
VERSION     AR052663.1  GI:5977525
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Iyer,R.P., Agrawal,S. and Tan,W.
  TITLE     Procedure for the solid phase synthesis of .sup.35 S-labeled
            oligonucleotides with 3H-1,2-benzodithiol-3-one-1,1-dioxide
  JOURNAL   Patent: US 5833944-A 3 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 8
AR052664
LOCUS       AR052664                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5833944.
ACCESSION   AR052664
VERSION     AR052664.1  GI:5977526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Iyer,R.P., Agrawal,S. and Tan,W.
  TITLE     Procedure for the solid phase synthesis of .sup.35 S-labeled
            oligonucleotides with 3H-1,2-benzodithiol-3-one-1,1-dioxide
  JOURNAL   Patent: US 5833944-A 4 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
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  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 9
AR072068
LOCUS       AR072068                  25 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 4 from patent US 5912332.
ACCESSION   AR072068
VERSION     AR072068.1  GI:7222956
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S., Habus,I. and Kandimalla,E.R.
  TITLE     Affinity-based purification of oligonucleotides using soluble
            multimeric oligonucleotides
  JOURNAL   Patent: US 5912332-A 4 15-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 10
AR080760
LOCUS       AR080760                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5968909.
ACCESSION   AR080760
VERSION     AR080760.1  GI:10007490
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S., Temsamani,J. and Zhao,Q.
  TITLE     Method of modulating gene expression with reduced immunostimulatory
            response
  JOURNAL   Patent: US 5968909-A 1 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 11
AR080761
LOCUS       AR080761                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 2 from patent US 5968909.
ACCESSION   AR080761
VERSION     AR080761.1  GI:10007491
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S., Temsamani,J. and Zhao,Q.
  TITLE     Method of modulating gene expression with reduced immunostimulatory
            response
  JOURNAL   Patent: US 5968909-A 2 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 12
AR080762
LOCUS       AR080762                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 3 from patent US 5968909.
ACCESSION   AR080762
VERSION     AR080762.1  GI:10007492
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S., Temsamani,J. and Zhao,Q.
  TITLE     Method of modulating gene expression with reduced immunostimulatory
            response
  JOURNAL   Patent: US 5968909-A 3 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 13
AR082591
LOCUS       AR082591                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5973136.
ACCESSION   AR082591
VERSION     AR082591.1  GI:10009311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
```

```
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 14
AR082592
LOCUS       AR082592                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 2 from patent US 5973136.
ACCESSION   AR082592
VERSION     AR082592.1  GI:10009312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 2 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 15
AR082593
LOCUS       AR082593                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 3 from patent US 5973136.
ACCESSION   AR082593
VERSION     AR082593.1  GI:10009313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 3 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 16
AR082594
LOCUS       AR082594                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 4 from patent US 5973136.
ACCESSION   AR082594
VERSION     AR082594.1  GI:10009314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 4 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 17
AR082595
LOCUS       AR082595                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 5 from patent US 5973136.
ACCESSION   AR082595
VERSION     AR082595.1  GI:10009315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 5 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 18
AR082596
LOCUS       AR082596                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 6 from patent US 5973136.
ACCESSION   AR082596
VERSION     AR082596.1  GI:10009316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 6 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN
```

```
  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 19
AR082597
LOCUS       AR082597                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 7 from patent US 5973136.
ACCESSION   AR082597
VERSION     AR082597.1  GI:10009317
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 7 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 20
AR082598
LOCUS       AR082598                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 8 from patent US 5973136.
ACCESSION   AR082598
VERSION     AR082598.1  GI:10009318
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 8 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 21
AR082599
LOCUS       AR082599                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 9 from patent US 5973136.
ACCESSION   AR082599
VERSION     AR082599.1  GI:10009319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 9 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 22
AR082600
LOCUS       AR082600                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 10 from patent US 5973136.
ACCESSION   AR082600
VERSION     AR082600.1  GI:10009320
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 10 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 23
AR082601
LOCUS       AR082601                 25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 11 from patent US 5973136.
ACCESSION   AR082601
VERSION     AR082601.1  GI:10009321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 11 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN
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  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 24
AR082602
LOCUS       AR082602                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 12 from patent US 5973136.
ACCESSION   AR082602
VERSION     AR082602.1  GI:10009322
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 12 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 25
AR082603
LOCUS       AR082603                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 13 from patent US 5973136.
ACCESSION   AR082603
VERSION     AR082603.1  GI:10009323
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 13 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 26
AR082604
LOCUS       AR082604                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 14 from patent US 5973136.
ACCESSION   AR082604
VERSION     AR082604.1  GI:10009324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 14 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 27
AR082605
LOCUS       AR082605                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 15 from patent US 5973136.
ACCESSION   AR082605
VERSION     AR082605.1  GI:10009325
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 15 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 28
AR082606
LOCUS       AR082606                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 16 from patent US 5973136.
ACCESSION   AR082606
VERSION     AR082606.1  GI:10009326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 16 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c      1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
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  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 29
AR082607
LOCUS       AR082607                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 17 from patent US 5973136.
ACCESSION   AR082607
VERSION     AR082607.1  GI:10009327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 17 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 30
AR082608
LOCUS       AR082608                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 18 from patent US 5973136.
ACCESSION   AR082608
VERSION     AR082608.1  GI:10009328
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 18 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 31
AR082609
LOCUS       AR082609                  25 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 19 from patent US 5973136.
ACCESSION   AR082609
VERSION     AR082609.1  GI:10009329
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Agrawal,S.
  TITLE     Inverted chimeric oligonucleotides
  JOURNAL   Patent: US 5973136-A 19 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 32
AR118312
LOCUS       AR118312                  25 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 157 from patent US 6140490.
ACCESSION   AR118312
VERSION     AR118312.1  GI:14099218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Biesecker,G. and Gold,L.
  TITLE     High affinity nucleic acid ligands of complement system proteins
  JOURNAL   Patent: US 6140490-A 157 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 33
AR206340
LOCUS       AR206340                  25 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 20 from patent US 6372427.
ACCESSION   AR206340
VERSION     AR206340.1  GI:21504912
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kandimalla,E.R. and Agrawal,S.
  TITLE     Cooperative oligonucleotides
  JOURNAL   Patent: US 6372427-A 20 16-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        2 a      13 c       1 g       9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 34
AX363485
LOCUS       AX363485                25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 1 from Patent WO0208420.
ACCESSION   AX363485
VERSION     AX363485.1  GI:18695600
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 1 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 35
AX363486
LOCUS       AX363486                25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 2 from Patent WO0208420.
ACCESSION   AX363486
VERSION     AX363486.1  GI:18695601
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 2 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 36
AX363487
LOCUS       AX363487                25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 3 from Patent WO0208420.
ACCESSION   AX363487
VERSION     AX363487.1  GI:18695602
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 3 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 37
AX363488
LOCUS       AX363488                25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 4 from Patent WO0208420.
ACCESSION   AX363488
VERSION     AX363488.1  GI:18695603
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 4 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a     13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 38
AX363489
LOCUS       AX363489                25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 5 from Patent WO0208420.
ACCESSION   AX363489
VERSION     AX363489.1  GI:18695604
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 5 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a      13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 39
AX363490
LOCUS       AX363490                 25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 6 from Patent WO0208420.
ACCESSION   AX363490
VERSION     AX363490.1  GI:18695605
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 6 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a      13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


RESULT 40
AX363491
LOCUS       AX363491                 25 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 7 from Patent WO0208420.
ACCESSION   AX363491
VERSION     AX363491.1  GI:18695606
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Agrawal,S., Diasio,R.B. and Zhang,Z.
  TITLE     A method of down-regulating gene expression
  JOURNAL   Patent: WO 0208420-A 7 31-JAN-2002;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        2 a      13 c      1 g      9 t
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 2.8;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCGCACCCATCTCTCTCCTTCT 22
          ||||||||||||||||||||||
Db      4 TCGCACCCATCTCTCTCCTTCT 25


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